

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:07:24 ; Search time 18 seconds

(without alignments)  
20.077 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1.RRMKMKX 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 369414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 57228

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/1aa/5A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/1aa/5B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/1aa/backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
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| 1          | 41    | 100.0       | 7      | 4     | US-09-346-847-2   |
| 2          | 41    | 100.0       | 7      | 4     | US-09-346-847-26  |
| 3          | 38    | 92.7        | 7      | 4     | US-09-346-847-6   |
| 4          | 38    | 92.7        | 7      | 4     | US-09-346-847-7   |
| 5          | 36    | 87.8        | 7      | 4     | US-09-346-847-9   |
| 6          | 35    | 85.4        | 7      | 4     | US-09-346-847-10  |
| 7          | 34    | 82.9        | 7      | 4     | US-09-346-847-8   |
| 8          | 33    | 80.5        | 7      | 4     | US-09-346-847-12  |
| 9          | 29    | 70.7        | 7      | 4     | US-09-346-847-13  |
| 10         | 28    | 68.3        | 7      | 4     | US-09-346-847-11  |
| 11         | 27    | 65.9        | 7      | 2     | US-08-968-676-135 |
| 12         | 26    | 63.4        | 6      | 3     | US-08-960-054A-19 |
| 13         | 26    | 63.4        | 6      | 3     | US-08-958-993A-19 |
| 14         | 26    | 63.4        | 6      | 4     | US-08-859-206A-8  |
| 15         | 26    | 63.4        | 6      | 4     | US-09-925-715-8   |
| 16         | 25.5  | 62.2        | 7      | 4     | US-09-346-847-14  |
| 17         | 25.5  | 62.2        | 7      | 4     | US-09-346-847-15  |
| 18         | 25    | 61.0        | 6      | 1     | US-07-841-997A-22 |
| 19         | 25    | 61.0        | 6      | 1     | US-08-290-301-22  |
| 20         | 25    | 61.0        | 6      | 4     | US-09-013-598-22  |
| 21         | 24    | 58.5        | 7      | 4     | US-08-584-043A-95 |
| 22         | 24    | 56.1        | 6      | 1     | US-07-851-941-6   |
| 23         | 23    | 56.1        | 6      | 1     | US-07-851-941-7   |
| 24         | 23    | 56.1        | 7      | 1     | US-08-182-175A-68 |
| 25         | 23    | 56.1        | 7      | 1     | US-08-182-175A-78 |
| 26         | 23    | 56.1        | 7      | 1     | US-08-474-633A-52 |
| 27         | 23    | 56.1        | 7      | 4     | US-08-823-771-52  |

|    |    |      |   |   |                   |                   |
|----|----|------|---|---|-------------------|-------------------|
| 28 | 23 | 56.1 | 7 | 5 | PCT-US92-06412-68 | Sequence 68, Appl |
| 29 | 23 | 56.1 | 7 | 5 | PCT-US92-06412-78 | Sequence 78, Appl |
| 30 | 22 | 53.7 | 5 | 3 | US-08-981-122-56  | Sequence 56, Appl |
| 31 | 22 | 53.7 | 6 | 3 | US-09-260-190-3   | Sequence 3, Appl  |
| 32 | 21 | 51.2 | 3 | 1 | US-08-433-037-14  | Sequence 14, Appl |
| 33 | 21 | 51.2 | 5 | 1 | US-07-657-769B-36 | Sequence 36, Appl |
| 34 | 21 | 51.2 | 5 | 1 | US-08-165-545-5   | Sequence 5, Appl  |
| 35 | 21 | 51.2 | 5 | 1 | US-08-256-771-14  | Sequence 14, Appl |
| 36 | 21 | 51.2 | 5 | 1 | US-07-789-184-97  | Sequence 97, Appl |
| 37 | 21 | 51.2 | 5 | 1 | US-08-433-037-6   | Sequence 6, Appl  |
| 38 | 21 | 51.2 | 5 | 1 | US-08-475-263-97  | Sequence 97, Appl |
| 39 | 21 | 51.2 | 5 | 1 | US-08-485-886-97  | Sequence 97, Appl |
| 40 | 21 | 51.2 | 5 | 1 | US-08-381-984-14  | Sequence 14, Appl |
| 41 | 21 | 51.2 | 5 | 2 | US-08-477-362-97  | Sequence 97, Appl |
| 42 | 21 | 51.2 | 5 | 2 | US-08-477-134-97  | Sequence 97, Appl |
| 43 | 21 | 51.2 | 5 | 3 | US-08-473-489A-97 | Sequence 97, Appl |
| 44 | 21 | 51.2 | 5 | 3 | US-08-485-695-97  | Sequence 97, Appl |
| 45 | 21 | 51.2 | 5 | 3 | US-08-981-122-27  | Sequence 27, Appl |

#### ALIGNMENTS

```
RESULT 1
US-09-346-847-2
; Sequence 2, Application US/09346847
; Patent No. 6472507
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/09/346,847
; CURRENT FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-346-847-2

Query Match          100.0%; Score 41; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. NO. 3e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 RRMKMKX 7
Db      1 RRMKMKX 7

RESULT 2
US-09-346-847-26
; Sequence 26, Application US/09346847
; Patent No. 6472507
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/09/346,847
; CURRENT FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
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TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (7)  
OTHER INFORMATION: AMIDATION  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-346-847-26

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
|:|||||  
Db 1 RRMKWK 7

RESULT 3  
US-09-346-847-6  
Sequence 6, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-6

Query Match 92.7%; Score 38; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
|:|||||  
Db 1 RRMKWK 7

RESULT 4  
US-09-346-847-7  
Sequence 7, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: peptide  
US-09-346-847-7

Query Match 92.7%; Score 38; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
|:|||||  
Db 1 RRMKWK 7

RESULT 5  
US-09-346-847-9  
Sequence 9, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 9  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-9

Query Match 87.8%; Score 36; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
|:|||||  
Db 1 RRMKWK 7

RESULT 6  
US-09-346-847-10  
Sequence 10, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 10  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (3)  
OTHER INFORMATION: Orn  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-10

Query Match 85.4%; Score 35; DB 4; Length 7;

Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
Db 1 RRMKMK 7

## RESULT 7

US-09-346-847-8  
; Sequence 8, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-8

Query Match 82.3%; Score 34; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
Db 1 RRMKMK 7

## RESULT 8

US-09-346-847-12  
; Sequence 12, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-12

Query Match 80.5%; Score 33; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
Db 1 RRMKMK 7

## RESULT 9

US-09-346-847-13  
; Sequence 13, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (2)\_"  
; OTHER INFORMATION: Orn  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-13

Query Match 70.7%; Score 29; DB 4; Length 7;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
Db 1 RRMKMK 7

## RESULT 10

US-09-346-847-11  
; Sequence 11, Application US/09346847  
; Patent No. 6472507  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/09/346,847  
; CURRENT FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-346-847-11

Query Match 68.3%; Score 28; DB 4; Length 7;  
Best Local Similarity 85.7%; Pred. No. 3e+05;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
Db 1 RRMKMK 7

## RESULT 11

US-08-968-676-135  
; Sequence 135, Application US/08968676

Patent No. 5919639  
GENERAL INFORMATION:  
APPLICANT: Humphreys, Robert E  
APPLICANT: Adams, Sharlene  
APPLICANT: Xu, Minzhen  
TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN  
NUMBER OF SEQUENCES: 165  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kevin W. Farrell, P.C.  
STREET: P.O. Box 999  
CITY: York Harbor  
STATE: ME  
COUNTRY: USA  
ZIP: 03911  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/968,676  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Farrell, Kevin M  
REGISTRATION NUMBER: 35,505  
REFERENCE/DOCKET NUMBER: REH-9601  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (207) 363-0558  
TELEFAX: (207) 363-0528  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-968-676-135

Query Match 65.9%; Score 27; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RKKKK 7  
DB 2 RKKKK 7

RESULT 12  
US-08-960-054A-19  
Sequence 19, Application US/08960054A  
Patent No. 6261537  
GENERAL INFORMATION:  
APPLICANT: Nycomed Imaging AS  
TITLE OF INVENTION: Improvements in or relating to  
TITLE OF INVENTION: diagnostic/therapeutic  
TITLE OF INVENTION: agents  
FILE REFERENCE: REF/Kiavness/054  
CURRENT APPLICATION NUMBER: US/08/960,054A  
CURRENT FILING DATE: 1997-10-29  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 19  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial  
OTHER INFORMATION: Sequence:lipopeptide  
NAME/KEY: MOD\_RES  
LOCATION: (1)\_Lys  
OTHER INFORMATION: Dipalmitoyl-Lys  
NAME/KEY: MOD\_RES

LOCATION: (5)  
OTHER INFORMATION: Biotinylated-Lys  
US-08-960-054A-19

Query Match 63.4%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKKK 7  
DB 1 KKKK 4

RESULT 13  
US-08-958-993A-19  
Sequence 19, Application US/08958993A  
Patent No. 6264917  
GENERAL INFORMATION:  
APPLICANT: Nycomed Imaging AS  
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
TITLE OF INVENTION: agents  
FILE REFERENCE: REF/Kiavness/993  
CURRENT APPLICATION NUMBER: US/08/958,993A  
CURRENT FILING DATE: 1997-10-28  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 19  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:lipopeptide  
NAME/KEY: MOD\_RES  
LOCATION: (1)  
OTHER INFORMATION: Dipalmitoyl-Lys  
NAME/KEY: MOD\_RES  
LOCATION: (5)  
OTHER INFORMATION: Biotinylated-Lys  
US-08-958-993A-19

Query Match 63.4%; Score 26; DB 3; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKKK 7  
DB 1 KKKK 4

RESULT 14  
US-08-959-206A-8  
Sequence 8, Application US/08959206A  
Patent No. 6331289  
GENERAL INFORMATION:  
APPLICANT: Nycomed Imaging AS  
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
TITLE OF INVENTION: agents  
FILE REFERENCE: REF/Kiavness/206  
CURRENT APPLICATION NUMBER: US/08/959,206A  
CURRENT FILING DATE: 1997-10-24  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 8  
LENGTH: 6  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:lipopeptide  
NAME/KEY: MOD\_RES  
LOCATION: (5)  
OTHER INFORMATION: Biotinylated-Lys  
NAME/KEY: MOD\_RES  
LOCATION: (1)

OTHER INFORMATION: Dipalmitoyl-lysine  
US-08-959-206A-8

Query Match 63.4%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWKK 7  
DB 1 KWKK 4

RESULT 15  
US-09-925-715-8  
; Sequence 8, Application US/0925715  
; Patent No. 668047  
; GENERAL INFORMATION:  
; APPLICANT: Mycomed Imaging AS  
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic  
; TITLE OF INVENTION: Agents  
; FILE REFERENCE: REF/Klavness/206  
; CURRENT APPLICATION NUMBER: US/09/925,715  
; CURRENT FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:lipopeptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Biocinylated-lys  
; NAME/KEY: MOD\_RES  
; LOCATION: (1)  
; OTHER INFORMATION: Dipalmitoyl-lysine  
US-09-925-715-8

Query Match 63.4%; Score 26; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWKK 7  
DB 1 KWKK 4

Search completed: August 11, 2004, 14:10:27  
Job time : 19 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:58:42 ; Search time 16 seconds  
(without alignments)  
42.084 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues  
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description               |
|------------|-------|-------------|--------|-------|---------------------------|
| 1          | 41    | 100.0       | 33     | 2     | S57235 antennapedia prote |
| 2          | 41    | 100.0       | 42     | 2     | I65241 homeotic protein H |
| 3          | 41    | 100.0       | 42     | 2     | I65249 homeoprotein 13A - |
| 4          | 41    | 100.0       | 45     | 2     | PC1216 homeotic protein D |
| 5          | 41    | 100.0       | 48     | 2     | I51439 homeobox protein - |
| 6          | 41    | 100.0       | 60     | 2     | PC2399 antennapedia-like  |
| 7          | 41    | 100.0       | 60     | 2     | PC2400 antennapedia-like  |
| 8          | 41    | 100.0       | 60     | 2     | S69227 homeotic protein H |
| 9          | 41    | 100.0       | 60     | 2     | I51437 homeotic protein H |
| 10         | 41    | 100.0       | 62     | 2     | B12391 homeotic protein H |
| 11         | 41    | 100.0       | 66     | 2     | S15536 homeotic protein H |
| 12         | 41    | 100.0       | 66     | 2     | S15538 homeotic protein H |
| 13         | 41    | 100.0       | 66     | 2     | S15534 homeotic protein H |
| 14         | 41    | 100.0       | 67     | 2     | B27471 homeotic protein R |
| 15         | 41    | 100.0       | 69     | 2     | S13785 homeotic protein m |
| 16         | 41    | 100.0       | 70     | 2     | B37042 homeotic protein H |
| 17         | 41    | 100.0       | 71     | 2     | UC1161 homeotic protein 3 |
| 18         | 41    | 100.0       | 71     | 2     | A60084 homeotic protein H |
| 19         | 41    | 100.0       | 74     | 2     | D34510 homeotic protein H |
| 20         | 41    | 100.0       | 75     | 2     | I51341 homeobox protein H |
| 21         | 41    | 100.0       | 75     | 2     | S58852 homeotic protein S |
| 22         | 41    | 100.0       | 76     | 2     | C43559 homeotic protein R |
| 23         | 41    | 100.0       | 78     | 2     | I51342 homeobox protein   |
| 24         | 41    | 100.0       | 81     | 2     | S47605 homeotic protein H |
| 25         | 41    | 100.0       | 81     | 2     | B29585 homeotic protein H |
| 26         | 41    | 100.0       | 81     | 2     | A25180 homeotic protein H |
| 27         | 41    | 100.0       | 82     | 2     | S08302 homeotic protein H |
| 28         | 41    | 100.0       | 83     | 2     | S47603 homeotic protein H |
| 29         | 41    | 100.0       | 83     | 2     | S50066 homeotic protein H |

|    |    |       |     |   |                           |
|----|----|-------|-----|---|---------------------------|
| 30 | 41 | 100.0 | 85  | 2 | I65198 homeotic protein H |
| 31 | 41 | 100.0 | 85  | 2 | A25472 homeotic protein H |
| 32 | 41 | 100.0 | 86  | 2 | A34510 homeotic protein H |
| 33 | 41 | 100.0 | 86  | 2 | U70489 homeotic protein Z |
| 34 | 41 | 100.0 | 86  | 2 | S08303 homeotic protein H |
| 35 | 41 | 100.0 | 87  | 2 | S00589 homeotic protein M |
| 36 | 41 | 100.0 | 88  | 2 | A03317 homeotic protein H |
| 37 | 41 | 100.0 | 95  | 2 | B32830 homeotic protein H |
| 38 | 41 | 100.0 | 96  | 2 | S08639 homeotic protein Z |
| 39 | 41 | 100.0 | 96  | 2 | A05266 homeotic protein H |
| 40 | 41 | 100.0 | 96  | 2 | A55278 homeotic protein H |
| 41 | 41 | 100.0 | 97  | 2 | C27176 homeotic protein H |
| 42 | 41 | 100.0 | 97  | 2 | A24779 homeotic protein m |
| 43 | 41 | 100.0 | 99  | 2 | A41605 homeotic protein H |
| 44 | 41 | 100.0 | 103 | 2 | A32167 homeotic protein H |
| 45 | 41 | 100.0 | 104 | 2 | D43559 homeotic protein H |

## ALIGNMENTS

RESULT 1  
S57235 antennapedia protein (clone p1105) - fruit fly (Drosophila pseudoobscura) (fragment)  
C:Species: Drosophila pseudoobscura  
C>Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 15-Oct-1999  
C/Accession: S57235  
R/Randazzo, F.M.; Seeger, M.A.; Huss, C.A.; Sweeney, M.A.; Cecil, J.K.; Kaufman, T.C.  
Genetics 133, 319-330, 1993  
A/Title: Structural changes in the antennapedia complex of Drosophila pseudoobscura.  
A/Reference number: S57224  
A/Accession: S57235  
A/Molecule type: DNA  
A/Residues: 1-33 <RAN>  
A/Cross-References: EMBL:X77711  
C/Genetics:  
A/Gene: FlyBase:Antp  
A/Cross-References: FlyBase:FBgn0012693  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:1-22/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 33;  
Best Local Similarity 100.0%; Pred. No. 0.36; 0; Indels 0; Gaps 0;  
Matches 7; Conservative

QY 1 RRMKWK 7  
16 RRMKWK 22  
Db

RESULT 2  
I65241 homeotic protein Hox-A - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C/Date: 27-Feb-1997 #sequence\_revision 27-Feb-1997 #text\_change 15-Oct-1999  
C/Accession: I65241  
R/Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
Biochem. Genet. 32, 351-360, 1994  
A/Title: Cloning of rat homeobox genes.  
A/Reference number: I52340; MUID:J5217128; PMID:7702549  
A/Accession: I65241  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-42 <RBS>  
A/Cross-References: GB:S76290; NID:913077  
C/Genetics:  
A/Gene: Hox-A; Hox-1  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F:1-40/Domain: Homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 42;

Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
|||||  
Db 34 RRMKMKK 40

RESULT 3  
165249  
homeoprotein 13A - rat (fragment)  
C/Species: Rattus sp. (rat)  
C/Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 05-Nov-1999  
C/Accession: 165249  
R/Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
Biochem. Genet. 32, 351-360, 1994  
A/Title: Cloning of rat homeobox genes.  
A/Reference number: 152340; PMID:95217128; PMID:7702549  
A/Accession: 165249  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-42 <RES>  
A/Cross-references: GB:S76307; NID:9913074; PIDN:AA33921.1; PID:9913075

Query Match 100.0%; Score 41; DB 2; Length 42;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
|||||  
Db 34 RRMKMKK 40

RESULT 4  
PC1216  
homeotic protein Dthbx1 - planarian (Dugesia tigrina) (fragment)  
C/Species: Dugesia tigrina  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 17-Oct-1997  
C/Accession: PC1216  
R/Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fiedlitz, W.; Enrillo  
Gene 121, 337-342, 1992  
A/Title: Homeoboxes in flatworms.  
A/Reference number: JCI386; PMID:93077050; PMID:1359988  
A/Accession: PC1216  
A/Molecule type: DNA  
A/Residues: 1-45 <OLIT>  
A/Cross-references: EMBL:X66822  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/1-45/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 45;  
Best Local Similarity 100.0%; Pred. No. 0.51;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
|||||  
Db 39 RRMKMKK 45

RESULT 5  
151439  
homeobox protein - African clawed frog (fragment)  
C/Species: Xenopus laevis (African clawed frog)  
C/Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 15-Oct-1999  
C/Accession: 151439  
R/LeRoy, P.; DeRobertis, E.M.  
Dev. Dyn. 194, 21-32, 1992  
A/Title: Effects of lithium chloride and retinoic acid on the expression of genes from t  
A/Reference number: 151439; PMID:93043517; PMID:1384809  
A/Accession: 151439  
A/Status: Preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA

A/Residues: 1-48 <LER>  
A/Cross-references: GB:M91587; NID:9214257; PIDN:AAA49750.1; PID:9214258  
C/Genetics:  
A/Gene: Hox2.2  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/1-27/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 48;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
|||||  
Db 21 RRMKMKK 27

RESULT 6  
PC2399  
antennapedia-like homeotic protein ABox 2 - sea squirt (Styela clava) (fragment)  
C/Species: Styela clava  
C/Date: 13-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 21-Jul-2000  
C/Accession: PC2399  
R/Ge, T.; Lee, H.; Tomlinson, C.R.  
Gene 147, 219-222, 1994  
A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c1  
A/Reference number: PC2399; PMID:95011617; PMID:7926803  
A/Accession: PC2399  
A/Molecule type: DNA  
A/Residues: 1-60 <GERT>  
A/Cross-references: GB:S73920; NID:9653714; PIDN:AA33061.2; PID:97387472  
A/Note: The authors translated the codon ATT for residue 47 as Glu  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
|||||  
Db 52 RRMKMKK 58

RESULT 7  
PC2400  
antennapedia-like homeotic protein AHox 3 - sea squirt (Styela plicata) (fragment)  
C/Species: Styela plicata  
C/Date: 26-Jun-1995 #sequence\_revision 14-Jul-1995 #text\_change 17-Oct-1997  
C/Accession: PC2400  
R/Ge, T.; Lee, H.; Tomlinson, C.R.  
Gene 147, 219-222, 1994  
A/Title: Identification of an antennapedia-like homeobox gene in the ascidians Styela c1  
A/Reference number: PC2399; PMID:95011617; PMID:7926803  
A/Accession: PC2400  
A/Molecule type: DNA  
A/Residues: 1-60 <GERT>  
A/Note: The authors translated the codon ATA for residue 47 as Glu  
C/Superfamily: unassigned homeobox proteins; homeobox homology  
C/Keywords: DNA binding; homeobox; nucleus; transcription regulation  
P/2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.66;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
|||||  
Db 52 RRMKMKK 58

RESULT 8



S09227  
 homeotic protein Htr-A2 - leech (Helobdella triseriatis) (fragment)  
 C:Species: Helobdella triseriatis  
 C>Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 24-Sep-1999  
 C:Accession: S09227  
 R:Mcdeen, C.J.; Kosteriken, R.G.; Matsumura, I.; Weisblat, D.A.  
 Nucleic Acids Res. 18, 1908, 1990  
 A:Title: Evidence for a new family of evolutionarily conserved homeobox genes.  
 A:Reference number: S09227; MUID:90245602; PMID:1970867  
 A:Accession: S09227  
 A:Molecule type: DNA  
 A:Residues: 1-60 <MED>  
 A:Cross-references: EMBL:X51752; NID:g9463; PIND:CAA3604.1; PID:e20267; PID:g1335706  
 A:Note: the authors translated the codon TTC for residue 14 as Leu  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 9  
 151437  
 homeotic protein Hox 2.4 - African clawed frog (fragment)  
 C:Species: Xenopus laevis (African clawed frog)  
 C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 24-Sep-1999  
 C:Accession: 151437  
 R:Bitner, D.  
 Dev. Dyn. 196, 11-24, 1993  
 A:Title: Characterization of the Xenopus Hox 2.4 gene and identification of control elem  
 A:Reference number: 151437; MUID:93326800; PMID:7916675  
 A:Accession: 151437  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-60 <BIT>  
 A:Cross-references: GB:M83947; NID:g214252; PIND:AAA49748.1; PID:g214253  
 C:Genetics:  
 A:Gene: Hox 2.4  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 60;  
 Best Local Similarity 100.0%; Pred. No. 0.66; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 10  
 B32391  
 homeotic protein Hox 2.4 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 08-Dec-1989 #sequence\_revision 08-Dec-1989 #text\_change 17-Oct-1997  
 C:Accession: B32391  
 R:Graham, A.; Papalopulu, N.; Krumlauf, R.  
 Cell 57, 367-378, 1989  
 A:Title: The murine and Drosophila homeobox gene complexes have common features of organ  
 A:Reference number: A32391; MUID:89249299; PMID:2566383  
 A:Accession: B32391  
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A:Molecule type: DNA  
 A:Residues: 1-62 <GRA>  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation

F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 62;  
 Best Local Similarity 100.0%; Pred. No. 0.68; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 11  
 S15536  
 homeotic protein Hox A7 - human (fragment)  
 N:Alternate names: homeotic protein Hox 1A  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C:Accession: S15536  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
 Genome 31, 745-756, 1989  
 A:Title: Organization of human Class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A:Accession: S15536  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-66 <BON>  
 C:Genetics:  
 A:Gene: GDB:HOXA7  
 A:Cross-references: GDB:120647; OMIM:142950  
 A:Map position: 7p15.3-7p15.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.72; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

RESULT 12  
 S15538  
 homeotic protein Hox A6 - human (fragment)  
 N:Alternate names: homeotic protein Hox 1B  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C:Accession: S15538  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
 Genome 31, 745-756, 1989  
 A:Title: Organization of human Class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A:Accession: S15538  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-66 <BON>  
 C:Genetics:  
 A:Gene: GDB:HOXA6  
 A:Cross-references: GDB:120648; OMIM:142951  
 A:Map position: 7p15.3-7p15.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.72; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 52 RRMKMKK 58

## RESULT 13

S15534  
 homeotic protein Hox C8 - human (fragment)  
 N:Alternate names: homeotic protein Hox 3A  
 C:Species: Homo sapiens (man)  
 C>Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 29-Aug-1997  
 C:Accession: S15534  
 R:Boncinelli, E.; Acampora, D.; Pannese, M.; d'Esposito, M.; Somma, R.; Gaudino, G.; Stc  
 Genome 31, 745-756, 1989  
 A:Title: Organization of human class I homeobox genes.  
 A:Reference number: S15036; MUID:90215256; PMID:2576652  
 A:Accession: S15534  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-66 <BON>  
 C:Genetics:  
 A:Gene: GDB:HOXC8  
 A:Cross-references: GDB:120668; OMIM:142970  
 A:Map position: 12q13.3-12q13.3  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.72;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
 |||||  
 Db 52 RRMKWK 58

## RESULT 14

B27471  
 homeotic protein R2 - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 17-Nov-2000  
 C:Accession: B27471; 165243  
 R:Palzon, M.; Sanderson, N.; Chung, S.Y.  
 Gene 54, 23-32, 1987  
 A:Title: Cloning and expression of rat homeo-box-containing sequences.  
 A:Reference number: A91576; MUID:87277429; PMID:2886401  
 A:Accession: B27471  
 A:Molecule type: DNA  
 A:Residues: 1-67 <PAL>  
 R:Sakoyama, Y.; Mizuta, I.; Ogasawara, N.; Yoshikawa, H.  
 Biochem. Genet. 32, 351-360, 1994  
 A:Title: Cloning of rat homeobox genes.  
 A:Reference number: 152340; MUID:95217128; PMID:7702549  
 A:Accession: 165243  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-42 <RES>  
 A:Cross-references: GB:S76296; NID:913079  
 C:Genetics:  
 A:Gene: Hox-A; Hox-1  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:1-40/Domain: homeobox homology (fragment) <HOX>

Query Match 100.0%; Score 41; DB 2; Length 67;  
 Best Local Similarity 100.0%; Pred. No. 0.73;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
 |||||  
 Db 34 RRMKWK 40

## RESULT 15

S13785

homeotic protein m31 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-Mar-1997 #sequence\_revision 09-May-1997 #text\_change 17-Oct-1997  
 C:Accession: S13785  
 R:Breier, G.; Bucan, M.; Francke, U.; Colberg-Poley, A.M.; Gruss, P.  
 EMBO J. 5, 2209-2215, 1986  
 A:Title: Sequential expression of murine homeo box genes during F9 EC cell differentiation  
 A:Reference number: S13785; MUID:87053860; PMID:2877873  
 A:Accession: S13785  
 A:Molecule type: DNA  
 A:Residues: 1-69 <BRE>  
 C:Genetics:  
 A:Map position: 15  
 C:Superfamily: unassigned homeobox proteins; homeobox homology  
 C:Keywords: DNA binding; homeobox; nucleus; transcription regulation  
 F:2-58/Domain: homeobox homology <HOX>

Query Match 100.0%; Score 41; DB 2; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 0.75;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
 |||||  
 Db 52 RRMKWK 58

Search completed: August 11, 2004, 14:02:15  
 Job time : 16 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:54:57 ; Search time 13 seconds  
(without alignments)

28.038 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1 RRMKMKK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID           | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 41    | 100.0       | 48     | 1 HXB6_XENLA | P31256 xenopus lae |
| 2          | 41    | 100.0       | 49     | 1 HXA5_SHEEP | Q28599 ovis aries  |
| 3          | 41    | 100.0       | 60     | 1 HMA2_HELTR | P17138 heliodella  |
| 4          | 41    | 100.0       | 67     | 1 HXA4_RAT   | P09635 rattus norv |
| 5          | 41    | 100.0       | 71     | 1 HXA7_SHEEP | Q28600 ovis aries  |
| 6          | 41    | 100.0       | 71     | 1 HXC5_NOTVI | P31262 notonitaim  |
| 7          | 41    | 100.0       | 74     | 1 HMG9_APIME | P15660 apis mellif |
| 8          | 41    | 100.0       | 75     | 1 HMSG_SALSA | P09636 salmo salar |
| 9          | 41    | 100.0       | 76     | 1 HXC4_RAT   | P18665 rattus norv |
| 10         | 41    | 100.0       | 78     | 1 HXA5_SALSA | P09637 salmo salar |
| 11         | 41    | 100.0       | 80     | 1 HXA4_LINSA | P81192 linus sang  |
| 12         | 41    | 100.0       | 81     | 1 HXS1_BRARE | P09613 brachydanio |
| 13         | 41    | 100.0       | 82     | 1 HXB5_CHICK | P14538 gallus gall |
| 14         | 41    | 100.0       | 84     | 1 HXB6_CHICK | P14539 gallus gall |
| 15         | 41    | 100.0       | 86     | 1 SCR_APIME  | P15659 apis mellif |
| 16         | 41    | 100.0       | 87     | 1 HXA4_SHEEP | Q28598 ovis aries  |
| 17         | 41    | 100.0       | 87     | 1 HXC5_XENLA | P09020 xenopus lae |
| 18         | 41    | 100.0       | 92     | 1 HXB8_RAT   | P18663 rattus norv |
| 19         | 41    | 100.0       | 93     | 1 HXB8_PIG   | P09078 sus scrofa  |
| 20         | 41    | 100.0       | 96     | 1 HXC6_BRARE | P15862 brachydanio |
| 21         | 41    | 100.0       | 105    | 1 HXA7_RAT   | P09634 rattus norv |
| 22         | 41    | 100.0       | 105    | 1 HXB4_BRARE | P22574 brachydanio |
| 23         | 41    | 100.0       | 108    | 1 HXC8_RAT   | P18666 rattus norv |
| 24         | 41    | 100.0       | 112    | 1 HXB7_RAT   | P18664 rattus norv |
| 25         | 41    | 100.0       | 133    | 1 BRX2_SHEEP | Q90002 ovis aries  |
| 26         | 41    | 100.0       | 148    | 1 HXA5_JAMMS | PS0208 ambystoma m |
| 27         | 41    | 100.0       | 153    | 1 HXC6_SHEEP | P49325 ovis aries  |
| 28         | 41    | 100.0       | 188    | 1 HXD8_CHICK | P23459 gallus gall |
| 29         | 41    | 100.0       | 207    | 1 BRX1_CHICK | Q9668 gallus gall  |
| 30         | 41    | 100.0       | 208    | 1 HXA7_HETFR | Q91a25 heterodontu |
| 31         | 41    | 100.0       | 209    | 1 HXA7_XENLA | P09071 xenopus lae |
| 32         | 41    | 100.0       | 217    | 1 HXB7_BOVIN | Q91a89 bos taurus  |
| 33         | 41    | 100.0       | 217    | 1 HXB7_HUMAN | P09629 homo sapien |

|    |    |       |     |              |                    |
|----|----|-------|-----|--------------|--------------------|
| 34 | 41 | 100.0 | 217 | 1 HXB7_MOUSE | P09024 mus musculu |
| 35 | 41 | 100.0 | 220 | 1 HB7A_XENLA | Q91771 xenopus lae |
| 36 | 41 | 100.0 | 220 | 1 HB7B_XENLA | P04476 xenopus lae |
| 37 | 41 | 100.0 | 222 | 1 HXC5_HUMAN | O00444 homo sapien |
| 38 | 41 | 100.0 | 222 | 1 HXC5_MOUSE | P32043 mus musculu |
| 39 | 41 | 100.0 | 224 | 1 HXB6_HUMAN | P17509 homo sapien |
| 40 | 41 | 100.0 | 224 | 1 HXB6_MOUSE | P09023 mus musculu |
| 41 | 41 | 100.0 | 225 | 1 BRX1_HUMAN | Q91bui homo sapien |
| 42 | 41 | 100.0 | 225 | 1 HXA7_HUMAN | Q91bui morone saxa |
| 43 | 41 | 100.0 | 228 | 1 BRX2_MOUSE | O08686 mus musculu |
| 44 | 41 | 100.0 | 228 | 1 HXB6_BRARE | P15861 brachydanio |
| 45 | 41 | 100.0 | 229 | 1 HXA6_HETFR | Q91a24 heterodontu |

## ALIGNMENTS

```

RESULT 1
HXB6_XENLA          STANDARD;          PRT;          48 AA.
ID   HXB6_XENLA
AC   P31256;
DT   01-JUL-1993 (Rel. 26, Created)
DR   01-JUL-1993 (Rel. 26, Last sequence update)
DI   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Homeobox protein Hox-B6 (X1Hox-2.2) (Fragment).
GN   HoxB6 OR X1Hox-2.2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RY   [1]
RP   SEQUENCE FROM N.A.
RA   MEDLINE=93043517; PubMed=1384609;
RX   Leroy P., de Robertis E.M.;
RT   "Effects of lithium chloride and retinoic acid on the expression of
RT   genes from the Xenopus laevis Hox 2 complex.";
RL   Dev. Dyn. 194:21-32(1992).
CC   -!- FUNCTION: Sequence-specific transcription factor which is part of
CC   a developmental regulatory system that provides cells with
CC   specific positional identities on the anterior-posterior axis.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- SIMILARITY: Belongs to the Antp homeobox family.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@sib-sib.ch).
CC   -----
CC   EMBL, M91587; AAA49750.1; -.
CC   PIR, I51439; I51439.
CC   InterPro, IPR001827; Antennapedia.
CC   InterPro, IPR001356; Homeobox.
CC   Pfam, PF00046; homeobox.1.
CC   PRINTS, PR00024; HOMEBOX.
CC   ProDom, PD000010; Homeobox.1.
CC   SMART, SM00388; HOX.1.
CC   PROSITE, PS00027; HOMEBOX_1; 1.
CC   PROSITE, PS00032; ANTENNAPEDIA; PARTIAL.
CC   PROSITE, PS00071; HOMEBOX_2; 1.
CC   KW   Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC   Transcription regulation.
CC   FT   NON_TER
CC   FT   DNA_BIND
CC   SQ   SEQUENCE 48 AA; 5716 MW; BC39E36822EDDD2A CRC64;
Query Match          100.0%; Score 41; DB 1; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RRMKWK 7  
DB 21 RRMKWK 27

## RESULT 2

HXA5\_SHEEP STANDARD; PRT; 49 AA.

ID HXA5\_SHEEP

AC 028599;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Homeobox protein Hox-A5 (Fragment).

GN HOXA5 OR HOXA-5.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

NCBI\_TaxID=9940;

OX [1]

RP SEQUENCE FROM N.A.

RA Roche P.J.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Sequence-specific transcription factor which is part of

CC a developmental regulatory system that provides cells with

CC specific positional identities on the anterior-posterior axis.

CC Also binds to its own promoter. Binds specifically to the motif:

CC 5'-GYNATTA(TG)Y-3'.

CC -1- SUBCELLULAR LOCATION: Nuclear.

CC -1- SIMILARITY: Belongs to the Anp homeobox family.

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CC

DR EMBL; U61978; AAB04754.1; -.

DR HSSP; P02833; IHOM.

DR InterPro; IPR001356; Homeobox.

DR Pfam; PF00046; homeobox.1.

DR PRINTS; PR00024; HOMEBOX.

DR ProDom; PD000010; Homeobox; 1.

DR SMART; SM00389; HOX; 1.

DR PROSITE; PS00027; HOMEBOX 1; 1.

DR PROSITE; PSS0071; HOMEBOX 2; 1.

KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;

KW Transcription regulation.

FT NON\_TER

FT DNA\_BIND

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OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;

OC Rhynchobdellida; Glossiphoniidae; Helobdella.

NCBI\_TaxID=6413;

OX [1]

RP SEQUENCE FROM N.A.

RA Wedeen C.J., Kostriken R.G., Matsunura I., Weisblat D.A.;

RT "Evidence for a new family of evolutionarily conserved homeobox

RT genes.";

RL Nucleic Acids Res. 18:1908-1908(1990).

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -1- SIMILARITY: Contains 1 homeobox domain.

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OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;

OC Rhynchobdellida; Glossiphoniidae; Helobdella.

NCBI\_TaxID=6413;

OX [1]

RP SEQUENCE FROM N.A.

RA Wedeen C.J., Kostriken R.G., Matsunura I., Weisblat D.A.;

RT "Evidence for a new family of evolutionarily conserved homeobox

RT genes.";

RL Nucleic Acids Res. 18:1908-1908(1990).

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -1- SIMILARITY: Contains 1 homeobox domain.

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OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;

OC Rhynchobdellida; Glossiphoniidae; Helobdella.

NCBI\_TaxID=6413;

OX [1]

RP SEQUENCE FROM N.A.

RA Wedeen C.J., Kostriken R.G., Matsunura I., Weisblat D.A.;

RT "Evidence for a new family of evolutionarily conserved homeobox

RT genes.";

RL Nucleic Acids Res. 18:1908-1908(1990).

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).

CC -1- SIMILARITY: Contains 1 homeobox domain.

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RL Biochem. Genet. 32:351-360(1994).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
CC -----
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CC -----
CC EMBL; M16808; -; NOT_ANNOTATED_CDS.
CC EMBL; S76296; -; NOT_ANNOTATED_CDS.
CC PIR; B27471; B27471.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRODOM; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00032; ANTENNAPEIDIA; PARTIAL.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS50071; HOMEBOX 2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC NON_TER 1 1 HOMEBOX.
CC DNA_BIND <1 42
CC NON_TER 67 67
CC SEQUENCE 67 AA; 8346 MW; 5BFDFEA93193780 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 67;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 34 RRMKWK 40

RESULT 5
HXAY_SHEEP
ID HXAY_SHEEP STANDARD; PRT; 71 AA.
AC Q28600;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A7 (Fragment).
GN HOXA7 OR HOXA-7.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Roche P.O.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC -----
CC EMBL; U61879; AAB04755.1; -.
CC HSSP; P02833; 9ANT.
CC InterPro; IPR001356; Homeobox.
CC InterPro; IPR000047; HTH_lamdrepressor.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRODOM; PD000010; HTHREPRESSR.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX 1; 1.
CC PROSITE; PS50071; HOMEBOX 2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC NON_TER 1 1 HOMEBOX.
CC DNA_BIND 4 63
CC NON_TER 71 71
CC SEQUENCE 71 AA; 8888 MW; 931049FAC1BAACB7 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 55 RRMKWK 61

RESULT 6
HXCS_NOTVT
ID HXCS_NOTVT STANDARD; PRT; 71 AA.
AC P31262;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-C5 (NvHox-3.4) (Fragment).
GN Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
OC Notophthalmus.
OX NCBI_TaxID=8316;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92290273; PubMed=1351019;
RA Belleville S., Beauchemin M., Tremblay M., Noiseux N., Savard P.;
RA "Homeobox-containing genes in the newt are organized in clusters
RA similar to other vertebrates.";
RL Gene 114:179-186(1992).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC -----
CC EMBL; M84001; AAA49397.1; ALT_INIT.
CC PIR; JC1161; JC1161.
CC HSSP; P02833; 1SAN.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRODOM; PD000010; Homeobox; 1.

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DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 4 63 HOMEBOX.
FT NON_TER 71
SQ SEQUENCE 71 AA; 8979 MW; 07999FDE8995BA2 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 71;
Best Local Similarity 100.0%; Pred. No. 0.37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 55 RRMKWK 61

RESULT 7
HMS0 APIME STANDARD; PRT; 74 AA.
AC P15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein H90 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megaloptera; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_Taxid=7460;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9009384; PubMed=2574865;
RA Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila."
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
DR EMBL; M29493; AAA27728.1; -.
DR PIR; D34510; D34510.
DR HSSP; P02833; 1HOM.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1
FT DNA_BIND 74 74 HOMEBOX.
FT NON_TER 81
SQ SEQUENCE 74 AA; 9263 MW; 5FC8FB4F23D3837 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 1 RRMKWK 7

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Db 59 RRMKWK 65

RESULT 8
HMSA SALSA STANDARD; PRT; 75 AA.
ID HMSA_SALSA
AC P09636;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Homeobox protein 512-A (Fragment).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_Taxid=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Fjose A., Molven A., Eiken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes
RT from Atlantic salmon."
RL Gene 62:141-152(1988).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -1- SIMILARITY: Contains 1 homeobox domain.
CC -----
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CC -----
DR EMBL; M18903; AAA49559.1; -.
DR PIR; I51341; I51341.
DR HSSP; P02833; 9ANT.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX 1; 1.
DR PROSITE; PS00071; HOMEBOX 2; 1.
KW Homeobox; DNA-binding; Developmental protein; Nuclear protein.
FT NON_TER 1
FT DNA_BIND 1 60 HOMEBOX.
FT NON_TER 75 75
SQ SEQUENCE 75 AA; 9330 MW; FC02C3672F35475D CRC64;

Query Match 100.0%; Score 41; DB 1; Length 75;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
Db 52 RRMKWK 58

RESULT 9
HXCA RAT STANDARD; PRT; 76 AA.
ID HXCA_RAT
AC P1865;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-C4 (R3) (Fragment).
GN HOXC4 OR HOXC-4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=89231502; PubMed=2907739;
RA Falzon M., Chung S.Y.; homeobox-containing genes is developmentally
RT regulated and tissue specific";
RL Development 103:601-610(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Predominantly spinal cord and kidney.
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
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DR EMBL: M37567; AAA41343.1; -
DR PIR: C43559; C43559.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEOBOX.
DR PRINTS: PR00031; HTHREPRESSR.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS0071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 11 70 HOMEOBOX.
SQ SEQUENCE 76 AA; 9293 MW; 5235F665C0672385 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.4; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 RRMKMKK 7
   |||||
Db 62 RRMKMKK 68

RESULT 10
HXAS_SALSA STANDARD; PRT; 78 AA.
ID ID HXAS_SALSA STANDARD; PRT; 78 AA.
AC P09637;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-A5 (S12-B) (Fragment).
GN HOXA5.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OC NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88226009; PubMed=2897318;
RA Jose A., Molven A., Biken H.G.;
RT "Molecular cloning and characterization of homeo-box-containing genes

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RT from Atlantic salmon."
RL Gene 62:141-152(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC
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-----
DR EMBL: M18904; AAA49560.1; -
DR PIR: I51342; I51342.
DR HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEOBOX.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEOBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS0071; HOMEOBOX_2; 1.
DR Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KW Transcription regulation.
FT NON_TER 1
FT DNA_BIND 1 60 HOMEOBOX.
SQ SEQUENCE 78 AA; 9489 MW; 828DEBDDP78AC820 CRC64;

Query Match 100.0%; Score 41; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.41; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 1 RRMKMKK 7
   |||||
Db 52 RRMKMKK 58

RESULT 11
HX44_LINSA STANDARD; PRT; 80 AA.
ID ID HX44_LINSA STANDARD; PRT; 80 AA.
AC P81192;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Homeobox protein Hox-A4 (Lshox 4) (Fragment).
GN HOXA4.
OS Linus sanguineus (Ribon worm).
OC Eukaryota; Metazoa; Nemertea; Anopla; Heteronemertea; Lineidae;
OC Linus.
OC NCBI_TaxID=48190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98169491; PubMed=9501210;
RA Kmita-Cunha M., Locoil F., Bierre J., Gehring W.J.;
RT "Homeobox genes in the ribon worm Linus sanguineus: evolutionary
RT implications."
RL Proc. Natl. Acad. Sci. U.S.A. 95:3030-3035(1998).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: Belongs to the Antp homeobox family. Deformed
CC subfamily.
CC HSSP: P02833; 9ANT.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.

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DR InterPro: IPR000047; HTH_lambdarepressr.
DR Pfam: PF00046; homeobox_1.
DR PRINTS: PR00024; HOMEBOX.
DR PRINTS: PR00031; KTHREPRESSR.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT NON_TER 1
FT DNA_BIND 21 80 HOMEBOX.
FT NON_TER 80
SQ SEQUENCE 80 AA; 9860 MW; F2CE1B01CB8042F1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 80;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
DB 62 RRMKWK 68

RESULT 12
HXB5_BRAE
ID HXB5_BRAE STANDARD; PRT; 81 AA.
AC P09013;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 like (ZF-54) (Fragment).
GN HOXB5 OR ZF54 OR ZF-54.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
SE SEQUENCE FROM N.A.
RA MEDLINE=8901617; PubMed=2902580;
RA Njolstad P.R., Mølven A., Hordvik I., Apold J., Fjose A.;
RT "Primary structure, developmentally regulated expression and
RT potential duplication of the zebrafish homeobox gene ZF-21.";
RL Nucleic Acids Res. 16:9097-9113(1988).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12803; CAA31291.1; -.
DR HSSP: P02833; ISAN.
DR ZFIN: ZDB-GENE-000823-6; hoxb5b.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT NON_TER 1

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FT DNA_BIND 6 65 HOMEBOX.
SQ SEQUENCE 81 AA; 9977 MW; B7698AEFFB3C6B4 CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
DB 57 RRMKWK 63

RESULT 13
HXB5_CHICK
ID HXB5_CHICK STANDARD; PRT; 82 AA.
AC P14838;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein Hox-B5 (Hox-2.1) (Fragment).
GN HOXB5 OR HOX-2.1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SE SEQUENCE FROM N.A.
RA TISUE=Erythrocyte;
RA MEDLINE=90162373; PubMed=2575515;
RA Wedden S.E., Pang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
RT embryogenesis.";
RL Development 105:639-650(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
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CC -----
DR EMBL: X16846; CAA34743.1; -.
DR PIR: S08302; S08302.
DR HSSP: P02833; ISAN.
DR InterPro: IPR001827; Antennapedia.
DR InterPro: IPR001356; Homeobox.
DR Pfam: PF00046; homeobox; 1.
DR PRINTS: PR00024; HOMEBOX.
DR PRODOM: PD00010; Homeobox; 1.
DR SMART: SM00389; HOX; 1.
DR PROSITE: PS00027; HOMEBOX_1; 1.
DR PROSITE: PS00032; ANTENNAPEDIA; PARTIAL.
DR PROSITE: PS00071; HOMEBOX_2; 1.
KM Homeobox; DNA-binding; Developmental protein; Nuclear protein;
KM Transcription regulation.
FT NON_TER 1
FT DNA_BIND 7 66 HOMEBOX.
FT NON_TER 66
SQ SEQUENCE 82 AA; 9877 MW; 53F70ACDC9FDEF8F CRC64;

Query Match
Best Local Similarity 100.0%; Score 41; DB 1; Length 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7
DB 58 RRMKWK 64

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RESULT 14
HXB6_CHICK STANDARD; PRT; 84 AA.
ID P14839;
AC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Homeobox protein Hox-B6 (HBOX-2.2) (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX NCBI_TaxID=9031;
RN SEQUENCE FROM N.A.
RC TISSUE=Erythrocyte;
RC MEDLINE=90126373; PubMed=2575515;
RA Medden S.E., Pang K., Eichele G.;
RT "Expression pattern of homeobox-containing genes during chick
RT embryogenesis.";
RL Development 105:639-650(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Belongs to the Antp homeobox family.
CC -----
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CC -----
CC EMBL; X16847; CAA34744.1; -.
CC PIR; S08303; S08303.
CC HSSP; P02833; 1HOM.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC PRINTS; PR00031; HTHREPRESSR.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein;
CC Transcription regulation.
CC NON_TER 1 1
CC DNA_BIND 7 66 HOMEBOX.
CC SEQUENCE 84 AA; 10279 MW; BC06B10165B19E71 CRC64;
SQ

```

```

Query Match 100.0%; Score 41; DB 1; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RRMKMKK 7
Db 58 RRMKMKK 64

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RESULT 15
SCR_APIME STANDARD; PRT; 86 AA.
ID P15859;
AC 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)

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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Homeobox protein H55 (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OC NCBI_TaxID=7460;
RX NCBI_TaxID=7460;
RN SEQUENCE FROM N.A.
RC MEDLINE=90093384; PubMed=2574865;
RC Walldorf U., Fleig R., Gehring W.J.;
RT "Comparison of homeobox-containing genes of the honeybee and
RT Drosophila.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:9971-9975(1989).
CC -1- FUNCTION: Sequence-specific transcription factor which is part of
CC a developmental regulatory system that provides cells with
CC specific positional identities on the anterior-posterior axis.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE ANTP HOMEBOX FAMILY. STRONGEST, TO SCR
CC OF DROSOPHILA.
CC -----
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CC -----
CC EMBL; M29488; AAA27723.1; -.
CC PIR; A34510; A34510.
CC HSSP; P02833; 1SAN.
CC InterPro; IPR001827; Antennapedia.
CC InterPro; IPR001356; Homeobox.
CC Pfam; PF00046; homeobox; 1.
CC PRINTS; PR00024; HOMEBOX.
CC ProDom; PD000010; Homeobox; 1.
CC SMART; SM00389; HOX; 1.
CC PROSITE; PS00032; ANTENNAPEDIA; PARTIAL.
CC PROSITE; PS00027; HOMEBOX_1; 1.
CC PROSITE; PS00071; HOMEBOX_2; 1.
CC Homeobox; DNA-binding; Developmental protein; Nuclear protein.
CC NON_TER 1 1
CC DNA_BIND 8 67 HOMEBOX.
CC SEQUENCE 86 AA; 10713 MW; 2A49AB857C138AB8 CRC64;
SQ

```

```

Query Match 100.0%; Score 41; DB 1; Length 86;
Best Local Similarity 100.0%; Pred. No. 0.45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RRMKMKK 7
Db 59 RRMKMKK 65

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Search completed: August 11, 2004, 14:01:01
Job time : 14 secs

```

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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:58:07; Search time 36 Seconds  
(without alignments)  
61.351 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPRMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriophage:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID  | Description         |
|------------|-------|-------------|--------|--------|---------------------|
| 1          | 41    | 100.0       | 30     | Q86FV5 | Q86FV5 lampetra fl  |
| 2          | 41    | 100.0       | 33     | Q86FV0 | Q86FV0 diosophila   |
| 3          | 41    | 100.0       | 39     | Q9XV68 | Q9XV68 canis fam1   |
| 4          | 41    | 100.0       | 39     | Q57368 | Q57368 brachydantio |
| 5          | 41    | 100.0       | 42     | Q80WH6 | Q80WH6 rattus sp.   |
| 6          | 41    | 100.0       | 43     | Q57359 | Q57359 brachydantio |
| 7          | 41    | 100.0       | 44     | Q86R21 | Q86R21 nematostell  |
| 8          | 41    | 100.0       | 46     | Q9PVR9 | Q9PVR9 oryzias lat  |
| 9          | 41    | 100.0       | 51     | Q27413 | Q27413 ctenodrilus  |
| 10         | 41    | 100.0       | 51     | Q23743 | Q23743 ctenodrilus  |
| 11         | 41    | 100.0       | 51     | Q26407 | Q26407 ctenodrilus  |
| 12         | 41    | 100.0       | 57     | Q9PVR8 | Q9PVR8 oryzias lat  |
| 13         | 41    | 100.0       | 58     | Q9Y188 | Q9Y188 priapulid c  |
| 14         | 41    | 100.0       | 58     | Q25208 | Q25208 junonia coe  |
| 15         | 41    | 100.0       | 58     | Q57362 | Q57362 brachydantio |
| 16         | 41    | 100.0       | 59     | Q86R21 | Q86R21 lithobius a  |

|    |    |       |    |        |                     |
|----|----|-------|----|--------|---------------------|
| 17 | 41 | 100.0 | 59 | Q9NB42 | Q9NB42 anopheles g  |
| 18 | 41 | 100.0 | 59 | Q9PVR5 | Q9PVR5 oryzias lat  |
| 19 | 41 | 100.0 | 60 | Q77143 | Q77143 archegozete  |
| 20 | 41 | 100.0 | 60 | Q77139 | Q77139 archegozete  |
| 21 | 41 | 100.0 | 60 | Q97219 | Q97219 brachylosto  |
| 22 | 41 | 100.0 | 60 | Q26375 | Q26375 styela claf  |
| 23 | 41 | 100.0 | 60 | Q80WH7 | Q80WH7 rattus sp.   |
| 24 | 41 | 100.0 | 60 | Q80WH4 | Q80WH4 rattus sp.   |
| 25 | 41 | 100.0 | 60 | Q80WH3 | Q80WH3 rattus sp.   |
| 26 | 41 | 100.0 | 60 | Q80WH2 | Q80WH2 rattus sp.   |
| 27 | 41 | 100.0 | 60 | Q9PVR2 | Q9PVR2 petromyzon   |
| 28 | 41 | 100.0 | 60 | Q86GL9 | Q86GL9 petromyzon   |
| 29 | 41 | 100.0 | 60 | Q86GL5 | Q86GL5 petromyzon   |
| 30 | 41 | 100.0 | 60 | Q86GL3 | Q86GL3 petromyzon   |
| 31 | 41 | 100.0 | 60 | Q86GL6 | Q86GL6 petromyzon   |
| 32 | 41 | 100.0 | 60 | Q86GL2 | Q86GL2 petromyzon   |
| 33 | 41 | 100.0 | 60 | Q91769 | Q91769 xenopus lae  |
| 34 | 41 | 100.0 | 60 | Q86GL8 | Q86GL8 petromyzon   |
| 35 | 41 | 100.0 | 60 | Q9PVR2 | Q9PVR2 petromyzon   |
| 36 | 41 | 100.0 | 60 | Q86GL7 | Q86GL7 petromyzon   |
| 37 | 41 | 100.0 | 61 | Q27910 | Q27910 polyanthra   |
| 38 | 41 | 100.0 | 63 | Q86KB2 | Q86KB2 holopneuste  |
| 39 | 41 | 100.0 | 63 | Q86KB2 | Q86KB2 holopneuste  |
| 40 | 41 | 100.0 | 66 | Q57356 | Q57356 brachydantio |
| 41 | 41 | 100.0 | 69 | Q963K9 | Q963K9 phascollon   |
| 42 | 41 | 100.0 | 69 | Q9U9T4 | Q9U9T4 nereis vire  |
| 43 | 41 | 100.0 | 69 | Q9BME7 | Q9BME7 halloctis as |
| 44 | 41 | 100.0 | 69 | Q9PVR3 | Q9PVR3 oryzias lat  |
| 45 | 41 | 100.0 | 70 | Q967W5 | Q967W5 folsomia ca  |

## ALIGNMENTS

|          |   |                                      |      |        |
|----------|---|--------------------------------------|------|--------|
| RESULT 1 | Q86FV5  | PRELIMINARY;                         | PRT; | 30 AA. |
| AC       | Q86FV5  | 01-JUN-2002 (TREMBLER1, 21, Created) |      |        |
| DT       | 01-JUN-2002 (TREMBLER1, 21, Last sequence update)   |                                      |      |        |
| DT       | 01-JUN-2003 (TREMBLER1, 24, Last annotation update)   |                                      |      |        |
| DE       | Homeobox protein Hox15 (Fragment)   |                                      |      |        |
| OS       | Lampetra fluviatilis (River lamprey)  |                                      |      |        |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperostea;                                       |                                      |      |        |
| OC       | Petromyzontiformes; Petromyzontidae; Lampetra.  |                                      |      |        |
| OX       | NCBI_taxid=7748;  |                                      |      |        |
| RN       | [1]   |                                      |      |        |
| RP       | SEQUENCE FROM N.A.  |                                      |      |        |
| RX       | MEDLINE=21918662; PubMed=11919618;  |                                      |      |        |
| RA       | Cohn M.J.;  |                                      |      |        |
| RL       | "Evolutionary biology: Lamprey Hox genes and the origin of jaws."                                     |                                      |      |        |
| RL       | Nature 416:386-387(2002).   |                                      |      |        |
| DR       | EMBL; AY089981; AAM09102.1; -   |                                      |      |        |
| DR       | GO; GO:0005634; C:nucleus; IEA.   |                                      |      |        |
| DR       | GO; GO:0003700; F:transcription factor activity; IEA.   |                                      |      |        |
| DR       | GO; GO:0006355; P:regulation of transcription; DNA-dependent; IEA.                                    |                                      |      |        |
| DR       | InterPro; IPR001356; Homeobox.  |                                      |      |        |
| DR       | PIfam; PF00046; homeobox_1.   |                                      |      |        |
| DR       | PROSITE; PS00071; HOMEBOX_2; 1.   |                                      |      |        |
| FT       | NON_TER   |                                      |      |        |
| FT       | SEQUENCE 30 AA; 3608 MM; 47882P581E5C8E0 CRC64;   |                                      |      |        |
| QY       | Query Match   | 100.0%; Score 41; DB 13; Length 30;  |      |        |
| DB       | Best local similarity 100.0%; Pred. No. 1; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |                                      |      |        |
| QY       | 1 RRMKWK 7  |                                      |      |        |
| DB       | 6 RRMKWK 12   |                                      |      |        |

RESULT 2  
Q86FV0

```

ID 086FU0 PRELIMINARY; PRT; 33 AA.
AC 086FU0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Antennapedia complex (Fragment).
GN ANT-C.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93292933; PubMed=8099892;
RA Randazzo F.M., Seeger M.A., Huss C.A., Sweeney M.A., Cecil J.K.,
RA Kaufman T.C.;
RT "Structural changes in the antennapedia complex of Drosophila
RT pseudoobscura."
RL Genetics 134:319-330(1993).
DR EMBL; S63455; AAPI3946.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR PRINTS; PR00024; HOMEBOX.
DR ProDom; PD000010; Homeobox; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR NON_TER 1
FT 33
SQ SEQUENCE 33 AA; 3863 MW; D78B37ED81PD45DF CRC64;

Query Match 100.0%; Score 41; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 16 RRMKKK 22

RESULT 3
QXRT68 PRELIMINARY; PRT; 39 AA.
ID 09XT68;
AC 09XT68;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hoxa (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99265967; PubMed=10331940;
RA Li R., Mignot E., Paraco J., Kadotani H., Cantanese J., Zhao B.,
RA Lin X., Hinton L., Ostrander E.A., Patterson D.F., de Jong P.T.;
RT "Construction and characterization of an eightfold redundant dog
RT genomic bacterial artificial chromosome library."
RL Genomics 58:9-17(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX Kadotani H., Mignot E.;
RA Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF103746; AAD40572.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.

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DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DE DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT 39
SQ SEQUENCE 39 AA; 4908 MW; 1252D75EA245BCAB CRC64;

Query Match 100.0%; Score 41; DB 6; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 22 RRMKKK 28

RESULT 4
QXRT68 PRELIMINARY; PRT; 39 AA.
ID 057368;
AC 057368;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Hoxc5 protein (Fragment).
DE HOXC5A OR HOXC5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk."
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14539; CAAT4874.1; -.
DR ZFIN; ZDB-GENE-980526-533; hoxc5a.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:transcription factor activity; IEA.
DR GO; GO:0003555; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR00047; HTH lambrerepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PROSITE; PS00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DE DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT 39
SQ SEQUENCE 39 AA; 4827 MW; 592A0FEC12558660 CRC64;

Query Match 100.0%; Score 41; DB 13; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7
DB 23 RRMKKK 29

RESULT 5
QXRT68 PRELIMINARY; PRT; 42 AA.
ID 080WH6;
AC 080WH6;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

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DE Hox-A|Hox-1 (Fragment).
GN HOX-A|HOX-1.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95217128; PubMed=7702549;
RA Sakayama Y., Mizuta I., Ogasawara N., Yoshikawa H.;
RT "Cloning of rat homeobox genes."
RL Biochem. Genet. 32:351-360 (1994).
DR EMBL; S76290; AABJ1864.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox_1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
FT NON_TER 1 42
FT SEQUENCE 42 AA; 5494 MW; 385E5153B92216FB9 CRC64;
SQ
Query Match 100.0%; Score 41; DB 11; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RRMKWK 7
DB 34 RRMKWK 40
RESULT 6
O57359 PRELIMINARY; PRT; 43 AA.
AC O57359;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hox5 protein (Fragment).
GN HOXB5 OR HOXA5.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
expression patterns in the trunk."
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14526; CAA74861.1; -
DR ZFIN; ZDB-GENE-000823-6; hoxb5b.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD00010; Homeobox; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 43
FT SEQUENCE 43 AA; 5050 MW; 53034C37F3DFA596 CRC64;
SQ

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Query Match 100.0%; Score 41; DB 13; Length 43;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RRMKWK 7
DB 19 RRMKWK 25
RESULT 7
O9GR21 PRELIMINARY; PRT; 44 AA.
AC O9GR21;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hox type homeodomain protein (Fragment).
GN ANTHOX1A.
OS Nematostella vectensis.
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;
OC Eukaryota; Metazoa; Chordata; Anthozoa; Zoantharia; Actinoptera;
OX NCBI_TaxID=45351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97435515; PubMed=9290214;
RA Finnerty J.R., Martindale M.O.;
RT "Homeoboxes in sea anemones (Cnidaria:Anthozoa): a PCR-based survey of
Nematostella vectensis and Metridium senile."
RL Biol. Bull. 193:62-76 (1997).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF020955; AAG37788.1; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRODOM; PD00010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
DR DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1 44
FT SEQUENCE 44 AA; 5362 MW; FAF8044070A9CCF3 CRC64;
SQ
Query Match 100.0%; Score 41; DB 5; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 RRMKWK 7
DB 20 RRMKWK 26
RESULT 8
O9PVR9 PRELIMINARY; PRT; 46 AA.
AC O9PVR9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE HOXA5A (Fragment).
GN HOXA5A.
OS Oryzias latipes (Medaka fish) (Japanese ricefish)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianchthyidae; Oryziatidae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kondo S., Naruse K., Shima A.;

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RT "Hox genes of the medakafish *Oryzias latipes*,"  
 RI Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: AB026960; BAA86243.1; -.  
 DR HSSP: P02833; 1HOM.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 46 AA; 5955 MW; 6039999ED4294DD3 CRC64;  
 Query Match 100.0%; Score 41; DB 13; Length 46;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKKKK 7  
 DB 32 RRMKKKK 38  
 RESULT 9  
 ID Q27413 PRELIMINARY; PRT; 51 AA.  
 AC Q27413;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE LOX5 ORTHOLOG homeobox (Fragment).  
 GN CTS-LOX5.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.  
 OX NCBI\_TaxID=40316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA Dick M.H., Buss L.W.;  
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
 (Annelida: Polychaeta).";  
 RL Mol. Phylogenet. Evol. 3:146-158(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dick M.H., Buss L.W.;  
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: U26629; AAC46851.1; -.  
 DR EMBL: 576226; AAC31777.1; -.  
 DR HSSP: P02833; 9ANT.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 51 AA; 6278 MW; 88C6F65161F94A22 CRC64;

Query Match 100.0%; Score 41; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKKKK 7  
 DB 32 RRMKKKK 38  
 RESULT 10  
 ID Q23743 PRELIMINARY; PRT; 51 AA.  
 AC Q23743;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Deformed ortholog homeobox (Fragment).  
 GN CTS-DFD.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.  
 OX NCBI\_TaxID=40316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA Dick M.H., Buss L.W.;  
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
 (Annelida: Polychaeta).";  
 RL Mol. Phylogenet. Evol. 3:146-158(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Dick M.H., Buss L.W.;  
 RT Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: U26629; AAC46849.1; -.  
 DR HSSP: P02833; 9ANT.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; P:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR PROSITE: PS00027; HOMEBOX 1; 1.  
 DR PROSITE: PS50071; HOMEBOX 2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 51 AA; 6533 MW; 9EDB50C927FBCBD5 CRC64;  
 Query Match 100.0%; Score 41; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKKKK 7  
 DB 32 RRMKKKK 38  
 RESULT 11  
 ID Q26407 PRELIMINARY; PRT; 51 AA.  
 AC Q26407;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE CTS-DFD protein (Fragment).  
 GN CTS-DFD.  
 OS Ctenodrilus serratus.  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Canalipalpata;  
 OC Terebellida; Ctenodrilidae; Ctenodrilus.

OX NCBI\_TaxID=40316;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94356262; PubMed=7915607;  
 RA Dick M.H., Buss L.W.,  
 RT "A PCR-based survey of homeobox genes in Ctenodrilus serratus  
 (Annelida: Polychaeta)."  
 RL Mol. Phylogenet. Evol. 3:146-158(1994).  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: S76416; AAB31775.1; -.  
 DR HSSP: P02833; 9ANT.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR InterPro: IPR000047; HTH\_lambdarepressr.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRODOM: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 51 AA; 653 MW; 9EDB50C9277FBCBD5 CRC64;  
 Query Match 100.0%; Score 41; DB 5; Length 51;  
 Best Local Similarity 100.0%; Pred. No. 1.8;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RRMKMKK 7  
 DB 32 RRMKMKK 38  
 RESULT 12  
 ID Q9PVR8 PRELIMINARY; PRT; 57 AA.  
 AC Q9PVR8;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE HOXA5A (Fragment).  
 GN HOXA5A.  
 OS Oryzias latipes (Medaka fish) (Japanese ricefish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;  
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kondo S., Naruse K., Shima A.,  
 RT "Hox genes of the medakafish Oryzias latipes."  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: AB026961; BAA86244.1; -.  
 DR HSSP: P02833; 1HOM.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRODOM: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 57 AA; 6891 MW; 5AA6430320F68C04 CRC64;

Query Match 100.0%; Score 41; DB 13; Length 57;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RRMKMKK 7  
 DB 32 RRMKMKK 38  
 RESULT 13  
 ID Q9Y188 PRELIMINARY; PRT; 58 AA.  
 AC Q9Y188;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Hb1 homeodomain protein (Fragment).  
 GN Hb1.  
 OS Priapulus caudatus.  
 OC Eukaryota; Metazoa; Priapulida; Priapulidae; Priapulidae.  
 OX NCBI\_TaxID=37621;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99318125; PubMed=10391241;  
 RA de Rosa R., Grenier J.K., Andreeva T., Cook C.E., Adoutte A., Akam M.,  
 RA Carroll S.B., Balavoine G.,  
 RT "Hox genes in brachiopods and priapulids and protostome evolution."  
 RL Nature 399:772-776(1999).  
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).  
 DR EMBL: AF144888; AAC04644.1; -.  
 DR HSSP: P02833; 9ANT.  
 DR GO: GO:0005634; C:nucleus; IEA.  
 DR GO: GO:0003700; F:transcription factor activity; IEA.  
 DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
 DR InterPro: IPR001356; Homeobox.  
 DR InterPro: IPR000047; HTH\_lambdarepressr.  
 DR Pfam: PF00046; homeobox; 1.  
 DR PRINTS: PR00024; HOMEBOX.  
 DR PRODOM: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 KW DNA-binding; Homeobox; Nuclear protein.  
 FT NON TER 1 1  
 SQ SEQUENCE 58 AA; 7323 MW; 572F30DA57C9A613 CRC64;  
 Query Match 100.0%; Score 41; DB 5; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 RRMKMKK 7  
 DB 33 RRMKMKK 39  
 RESULT 14  
 ID Q25208 PRELIMINARY; PRT; 58 AA.  
 AC Q25208;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Antennapedia protein (Fragment).  
 GN ANTENNAPEDIA.  
 OS Junonia coenia (Peacock butterfly) (Precis coenia).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Papilionidea; Nymphalidae; Nymphalinae; Junonia.  
 OX NCBI\_TaxID=39708;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95075456; PubMed=7840822;

```

RA  Warren R.W., Nagy L., Selegue J., Gates J., Carroll S.,
RT  "Evolution of homeotic gene regulation and function in flies and
RT  butterflies."
RL  Nature 372:458-461 (1994).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR  EMBL; L42135; AA68461.1; -.
DR  PIR; S58850; S58850.
DR  HSSP; P02833; 1HOM.
DR  GO; GO:0005634; C:nucleus; IEA.
DR  GO; GO:0003700; P:regulation of transcription factor activity; IEA.
DR  GO; GO:0003700; P:regulation of transcription, DNA-dependent; IEA.
DR  InterPro; IPR001356; Homeobox.
DR  InterPro; IPR000047; HTH_lambdarepressr.
DR  Pfam; PF00046; homeobox; 1.
DR  PRINTS; PR00024; HTHREPRESSR.
DR  PRINTS; PR00031; HTHREPRESSR.
DR  ProDom; PD000010; Homeobox; 1.
DR  SMART; SM00388; HOX; 1.
DR  PROSITE; PS00027; HOMEBOX_1; 1.
DR  PROSITE; PS00071; HOMEBOX_2; 1.
KW  DNA-binding; Homeobox; Nuclear protein.
FT  NON_TER 1
FT  NON_TER 58
SQ  SEQUENCE 58 AA; 7583 MW; BD69B4875BAE565E CRC64;

Query Match 100.0%; Score 41; DB 5; Length 58;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 RRMKWK 7
    |||||
DB  52 RRMKWK 58

RESULT 15
ID 057362 PRELIMINARY; PRT; 58 AA.
AC 057362;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hoxb7 protein (Fragment).
OS HOXB7A OR HOXB7.
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince V.E., Joly L., Ekker M., Ho R.K.;
RT "Zebrafish hox genes: genomic organization and modified colinear
RT expression patterns in the trunk";
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; Y14533; CAAT4868.1; -.
DR TRANSFAC; T03635; -.
DR ZFIN; ZDB-GENE-000329-2; hoxb7a.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; P:regulation of transcription factor activity; IEA.
DR GO; GO:0003700; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lambdarepressr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00388; HOX; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
FT NON_TER 1
FT NON_TER 58
SQ SEQUENCE 58 AA; 6863 MW; 41EA6F1448DA1E5 CRC64;

```

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Query Match 100.0%; Score 41; DB 13; Length 58;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY  1 RRMKWK 7
    |||||
DB  23 RRMKWK 29

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Search completed: August 11, 2004, 14:01:48
Job time : 37 secs

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CC amino acid substitutions. See GENESEQ records AAY83520-Y83581  
 XX Sequence 7 AA;  
 Query Match 100.0%; Score 41; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7

RESULT 2  
 ADE14786  
 ID ADE14786 standard; peptide; 7 AA.  
 XX ADE14786;  
 AC ADE14786;  
 DT 29-JAN-2004 (first entry)  
 DE Carrier moiety SeqID26 related to improved drug delivery.  
 XX drug delivery system; carrier group; homeobox peptide; drug metabolism;  
 KM drug biotransformation; drug excretion; drug half life; drug solubility;  
 KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
 KM fruit fly; mutant; mutain.  
 XX  
 OS Synthetic.  
 OS Drosophila melanogaster.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1 /note= "Optionally C-terminal H"  
 FT Modified-site 7 /note= "N-terminal amide"  
 FT  
 FT  
 PN W0200001417-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 22-JUN-1999; 99WO-GB001957.  
 XX  
 PR 03-JUL-1998; 98GB-00014527.  
 XX  
 PA (CYCL-) CYCLACEL LTD.  
 XX  
 PI Fischer PM, Wang S;  
 XX  
 DR WPI; 2000-160729/14.  
 XX  
 PT Delivery systems with improved delivery into target cells, half-life,  
 PT solubility in biological fluids, enhanced metabolism, biotransformation and  
 PT excretion, and minimal toxic side-effects.  
 XX  
 PS Claim 33; SEQ ID NO 26; 114pp; English.  
 XX  
 CC This invention relates to novel drug delivery systems comprising a drug  
 CC group linked to a carrier group comprising a homeobox peptide, its  
 CC fragment or derivative. The invention may provide a method of improved  
 CC delivery into target cells with enhanced metabolism, biotransformation and  
 CC excretion of a drug. The drug may be therapeutically active in both  
 CC intact and dissociated states. The invention may improve half-life of a  
 CC drug in human or animal bodies, improve solubility in biological fluids,  
 CC minimise known toxic or non-desirable side-effects, enhance onset of  
 CC action of a desired therapeutic effect, provide alternative routes for  
 CC administration of drug and decrease incidence of drug resistance. The  
 CC present sequence is the amino acid sequence of a carrier peptide derived  
 CC from penatrin, a peptide derived from the antennapedia homeodomain of  
 CC Drosophila melanogaster. The drug and carrier moieties associated with  
 CC this sequence in the exemplification of the invention are featured.  
 XX  
 SO Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7

RESULT 3  
 ADE14762  
 ID ADE14762 standard; peptide; 7 AA.  
 XX ADE14762;  
 AC ADE14762;  
 DT 29-JAN-2004 (first entry)  
 DE Drosophila melanogaster homeodomain truncated penatrin peptide SeqID2.  
 XX drug delivery system; carrier group; homeobox peptide; drug metabolism;  
 KM drug biotransformation; drug excretion; drug half life; drug solubility;  
 KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
 KM fruit fly.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN W0200001417-A1.  
 XX  
 PD 13-JAN-2000.  
 XX  
 PF 22-JUN-1999; 99WO-GB001957.  
 XX  
 PR 03-JUL-1998; 98GB-00014527.  
 XX  
 PA (CYCL-) CYCLACEL LTD.  
 XX  
 PI Fischer PM, Wang S;  
 XX  
 DR WPI; 2000-160729/14.  
 XX  
 PT Delivery systems with improved delivery into target cells, half-life,  
 PT solubility in biological fluids, enhanced metabolism, biotransformation and  
 PT excretion, and minimal toxic side-effects.  
 XX  
 PS Claim 9; SEQ ID NO 2; 114pp; English.  
 XX  
 CC This invention relates to novel drug delivery systems comprising a drug  
 CC group linked to a carrier group comprising a homeobox peptide, its  
 CC fragment or derivative. The invention may provide a method of improved  
 CC delivery into target cells with enhanced metabolism, biotransformation and  
 CC excretion of a drug. The drug may be therapeutically active in both  
 CC intact and dissociated states. The invention may improve half-life of a  
 CC drug in human or animal bodies, improve solubility in biological fluids,  
 CC minimise known toxic or non-desirable side-effects, enhance onset of  
 CC action of a desired therapeutic effect, provide alternative routes for  
 CC administration of drug and decrease incidence of drug resistance. The  
 CC present sequence is the amino acid sequence of a truncated form of  
 CC penatrin, a peptide derived from the antennapedia homeodomain of  
 CC Drosophila melanogaster, which is related to the invention.  
 XX  
 SO Sequence 7 AA;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7

RESULT 4  
 Query Match 100.0%; Score 41; DB 3; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKMKK 7  
 DB 1 RRMKMKK 7



AA048627  
ID AA048627 standard; peptide; 7 AA.  
XX  
AC AA048627;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 130.  
XX  
KW Antinflammatory; antiaesthetic; cytosolic; antiproliferative; neurotrophic;  
KW antineuritic; antineuritic; osteoplastic; antibacterial; vitruvian;  
KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
KW allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
PS Claim 11; Page 62; 88pp; English.  
XX  
CC The invention relates to an antinflammatory compound (especially  
CC AA048628-AA048645), comprising a membrane translocation domain (AA048620-  
CC AA048627 or AA048646-AA048651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AA048525-AA048619). The  
CC antinflammatory compounds have antipathic, cytosolic, antiproliferative,  
CC antineuritic, antineuritic, osteoplastic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, neurotrophic,  
CC antithrombotic, vitruvian and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, buritis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKXK 7  
|||||||

DB 1 RRMKXK 7  
RESULT 7  
AA048620  
ID AA048620 standard; peptide; 7 AA.  
XX  
AC AA048620;  
XX  
DT 20-MAR-2002 (first entry)  
XX  
DE Anti-inflammatory peptide SEQ ID NO 123.  
XX  
KW Antinflammatory; antiaesthetic; cytosolic; antiproliferative; neurotrophic;  
KW antineuritic; antineuritic; osteoplastic; antibacterial; vitruvian;  
KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
KW allergic; membrane translocation domain; NEMO binding domain; eczema;  
KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
KW autoimmune disorder; multiple sclerosis; transplant rejection;  
KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
XX  
OS Synthetic.  
XX  
PN WO200183554-A2.  
XX  
PD 08-NOV-2001.  
XX  
PF 02-MAY-2001; 2001WO-US014346.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PR 22-AUG-2000; 2000US-00643260.  
XX  
PA (PRAE-) PRAECIS PHARM INC.  
XX  
PA (UYVA) UNIV YALE.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K;  
XX  
DR WPI; 2002-121889/16.  
XX  
PT Novel antinflammatory compound comprising membrane translocation domain  
PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
PT activation, and for treating asthma, lung inflammation, psoriasis.  
XX  
PS Claim 11; Page 62; 88pp; English.  
XX  
CC The invention relates to an antinflammatory compound (especially  
CC AA048628-AA048645), comprising a membrane translocation domain (AA048620-  
CC AA048627 or AA048646-AA048651) which comprises from 6-15 amino acid  
CC residues, fused to a NEMO binding sequence (AA048525-AA048619). The  
CC antinflammatory compounds have antipathic, cytosolic, antiproliferative,  
CC antineuritic, antineuritic, osteoplastic, antibacterial,  
CC immunosuppressive, dermatological, neuroprotective, neurotrophic,  
CC antithrombotic, vitruvian and antiallergic activity. The compounds  
CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
CC domain that results in inhibition of IKKbeta kinase activation and  
CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
CC bowel disease, sepsis, vasculitis, buritis; autoimmune diseases such as  
CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
CC viral infections; and ataxia telangiectasia. The compounds are also  
CC useful for treating pro-inflammatory responses such as allergies,  
CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
CC sunburn, aging and arthritis  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 8  
ABP60478

ID ABP60478 standard; peptide; 7 AA.

ABP60478;

10-MAY-2003 (first entry)

NLS peptide SEQ ID NO 17.

Protease; detection; drug screening; caspase; apoptosis; infection;

nuclear localisation signal; NLS.

Unidentified.

WO2003012393-A2.

13-FEB-2003.

30-JUL-2002; 2002WO-US024119.

31-JUL-2001; 2001US-0309312P.

(CLON-) CLONTECH LAB INC.

Haugwitz M;

WPI; 2003-248202/24.

PT Detecting the presence of active protease in a cell for use in protease  
PT activity detection and drug screening applications, by using a protease  
PT detection fusion protein.

PS Disclosure; Page 10; 43pp; English.

XX The invention relates to a cell comprising a protease detection fusion  
CC protein containing first and second subcellular localisation domains (D1,  
CC D2) separated by a cleavage domain (CD) recognised by the protease,  
CC (where D1 is dominant over D2 and a label domain is present between CD  
CC and D2). The fusion protein is maintained for a period of time sufficient  
CC for CD to be cleaved by protease if present in the cell and subcellular  
CC location of label domain is detected. The method is useful for  
CC determining whether a cell contains an active protease. The method finds  
CC applications, including monitoring activity of a protease in a cell,  
CC monitoring the effect of an agent on the activity of a protease, e.g. for  
CC drug screening applications to identify agents that modulate the activity  
CC of a particular protease and studying the effect of a factor on  
CC expression of the protease-encoding gene. Detecting protease activity of  
CC interest in a cell is useful for determining the particular state of the  
CC cell associated with the particular protease, e.g. certain active  
CC caspases indicate that a cell is undergoing an apoptotic event. Protease  
CC detection applications can be used in diagnostic applications, including  
CC diagnosis of bacterial and/or viral pathogenic infection. The present  
CC sequence is that of a nuclear localisation signal (NLS) containing  
CC peptide disclosed in illustrations of the invention  
XX

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 9

ID ABP96972 standard; peptide; 7 AA.

ABP96972;

17-JUN-2003 (first entry)

Anti-inflammatory polypeptide SEQ ID NO:11.

XX Anti-inflammatory; inflammatory disorder; polybasic; antiallergic;  
XX cytostatic; tuberculostatic; nephrotoxic; antihemorrhagic; antiallergic;  
XX dermatological; immunosuppressive; antiallergic; antiparasitic; asthma;  
XX gynaecological; ophthalmological; thrombolytic; protein therapy;  
XX lung inflammation; cancer; chronic granulomatous disease; tuberculosis;  
XX leprosy; sarcoidosis; silicosis; nephritis; rheumatoid arthritis;  
XX amyloidosis; ankylosing spondylitis; chronic bronchitis; scleroderma;  
XX lupus; appendicitis; psoriasis; pelvic inflammatory disease; allergy;  
XX orbital inflammatory disease; thrombotic disease.

Synthetic.

WO2003020213-A2.

13-MAR-2003.

27-AUG-2002; 2002WO-US027421.

30-AUG-2001; 2001US-0316328P.

(PRAE-) PRAECTIS PHARM INC.

Lazarus D; Hannig G;

WPI; 2003-354457/33.

PT New polypeptide useful for treating inflammatory disorders, such as  
PT asthma, lung inflammation, cancer, chronic granulomatous diseases,  
PT nephritis, amyloidosis, rheumatoid arthritis, scleroderma or allergies.

PS Claim 34; Page 23; 35pp; English.

XX The present invention describes an anti-inflammatory compound comprising  
CC a polybasic peptide (I). (I) comprises the structure: B1-X1-X2-X3-B2-X4-  
CC X5-B3; or B1-X1-X2-B2-B3-X3-X4-B4, where B1, B2, B3 and B4 = basic amino  
CC acid residues; and X1, X2, X3, X4 and X5 = alpha-helix promoting amino  
CC residues. Also described: (1) methods of treating an inflammatory  
CC disorder in a subject; and (2) a method for modulating the secretion of  
CC pro-inflammatory cytokines in a cell. (1) has cytostatic,  
CC antiinflammatory, antiallergic, dermatological, immunosuppressive,  
CC antihemorrhagic, antiparasitic, gynaecological, ophthalmological and  
CC thrombolytic activities, and can be used in protein therapy. The  
CC composition and method are useful in treating inflammatory disorders,  
CC such as asthma, lung inflammation, cancer, chronic granulomatous diseases  
CC (e.g. tuberculosis, leprosy, sarcoidosis or silicosis), nephritis,  
CC amyloidosis, rheumatoid arthritis, ankylosing spondylitis, chronic  
CC bronchitis, scleroderma, lupus, appendicitis, psoriasis, pelvic  
CC inflammatory disease, orbital inflammatory disease, thrombotic disease  
CC and allergies. The present sequence represents a specifically claimed  
CC anti-inflammatory polypeptide from the present invention  
XX

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

|                       |   |               |
|-----------------------|---|---------------|
| AC                    |   | ADA61896;     |
| XX                    |   |               |
| DT                    | 20-NOV-2003   | (first entry) |
| XX                    |   |               |
| DE                    | NFKB.essential modulator (NEMO) binding peptide #96.                      |               |
| XX                    |   |               |
| KW                    | NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;                 |               |
| KM                    | antiinflammatory; antiasthmatic; antipsoriatic; antirheumatic;            |               |
| KW                    | antiarthritis; osteopathic; antibacterial; immunosuppressive;             |               |
| KM                    | dermatological; neuroprotective; cyostatic; motropic; vitruide;           |               |
| KW                    | gene therapy; anti-inflammatory; inflammatory disorder; asthma;           |               |
| KM                    | psoriasis; rheumatoid arthritis; osteoarthritis;                          |               |
| KW                    | inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;       |               |
| KM                    | systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;   |               |
| KW                    | Alzheimer's disease; viral infection; NF-kappa B essential modulator;     |               |
| XX                    | necrosis factor kappa B essential modulator.                              |               |
| OS                    | Unidentified.   |               |
| XX                    |   |               |
| PN                    | US2003054999-A1.  |               |
| XX                    |   |               |
| PD                    | 20-MAR-2003.  |               |
| XX                    |   |               |
| PF                    | 02-MAY-2001; 2001US-00847946.   |               |
| XX                    |   |               |
| PR                    | 02-MAY-2000; 2000US-0201261P.   |               |
| XX                    |   |               |
| PA                    | (MAYM/) MAY M J.  |               |
| PA                    | (GHOS/) GHOSH S.  |               |
| PA                    | (FIND/) FINDEIS M A.  |               |
| PA                    | (PHIL/) PHILLIPS K.   |               |
| PA                    | (HANN/) HANNIG G.   |               |
| XX                    |   |               |
| PI                    | May MD, Ghosh S, Findeis MA, Phillips K, Hannig G;                        |               |
| XX                    |   |               |
| DR                    | WPI; 2003-596541/56.  |               |
| XX                    |   |               |
| PT                    | New compound for diagnosing or treating inflammatory disorders, e.g.      |               |
| PT                    | cancer, psoriasis, rheumatoid arthritis, inflammatory bowel disease or    |               |
| PT                    | carcinoma, comprises a membrane translocation domain and a NEMO binding   |               |
| PT                    | sequence.   |               |
| PS                    | Claim 11; Page 24; 37pp; English.   |               |
| XX                    |   |               |
| CC                    | The invention describes an anti-inflammatory compound comprising (I). The |               |
| CC                    | compound is useful for diagnosing or treating inflammatory disorders,     |               |
| CC                    | such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,          |               |
| CC                    | inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g. |               |
| CC                    | systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis   |               |
| CC                    | Alzheimer's disease or viral infection. This is the amino acid sequence   |               |
| CC                    | of an anti-inflammatory peptide that binds to, and down-regulates,        |               |
| CC                    | necrosis factor kappa B (NFKB) essential modulator (NEMO).                |               |
| XX                    |   |               |
| SQ                    | Sequence 7 AA:  |               |
| QY                    |   |               |
| DB                    |   |               |
| Query Match           | 100.0%; Score 41; DB 6; Length 7;   |               |
| Best Local Similarity | 100.0%; Pwd. No. 1.4e+06;   |               |
| Matches               | 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.                        |               |
| I                     | RRMKWK 7  |               |
|                       |   |               |
|                       |   |               |
|                       |   |               |
|                       |   |               |
| 1                     | RRMKWK 7  |               |
| RESULT 12             |   |               |
| ID                    | ADCC22330 standard; peptide; 7 AA.  |               |
| XX                    |   |               |
| AC                    | ADCC22330;  |               |
| XX                    |   |               |
| DT                    | 18-DEC-2003 (first entry)   |               |
| XX                    |   |               |
| DE                    | Nuclear localisation signal motif amino acid sequence SEQ ID NO:179.      |               |

XX recombinant fusion protein; fusion protein; binding; detection;  
 KW localisation domain; binding domain;  
 KW subcellular compartment localisation.  
 OS Unidentified.  
 XX WO2003012068-A2.  
 XX PD 13-FEB-2003.  
 XX PF 01-AUG-2002; 2002WO-US024572.  
 XX PR 01-AUG-2001; 2001US-0309395P.  
 XX PR 13-DEC-2001; 2001US-0341589P.  
 XX PA (CELL-) CELLONICS INC.  
 XX PI Bright G, Premkumar DR, Chen Y;  
 XX DR WPI; 2003-248174/24.  
 XX PT New recombinant fusion protein comprising detection and first  
 PT localisation domains and a binding domain for the molecule of interest.  
 PT useful for detecting binding of a molecule of interest.  
 PS Claim 20; SEQ ID NO 179; 101pp; English.  
 XX  
 CC The present invention describes a recombinant fusion protein (1) for  
 CC detecting binding of a molecule of interest (1) comprising: (a) a  
 CC detection domain; (b) a first localisation domain; and (c) a binding  
 CC domain for the molecule of interest. The detection domain, the first  
 CC localisation domain and the binding domain for the molecule of interest  
 CC constituting the recombinant fusion protein for detecting binding of a  
 CC molecule of interest are operably linked. The binding domain for the  
 CC molecule of interest is separated from the first localisation domain by 0  
 CC -20 amino acid residues. The first localisation domain and the binding  
 CC domain for the molecule of interest both do not occur in a single non-  
 CC recombinant protein with the same spacing as in the recombinant fusion  
 CC protein for detecting binding of a molecule of interest. Also described:  
 CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;  
 CC (2) a recombinant expression vector comprising the nucleic acid control  
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a  
 CC genetically engineered host cell transfected with the recombinant  
 CC expression vector; (4) a kit for detecting binding of the molecule of  
 CC interest; and (5) a method for identifying compounds that alter the  
 CC binding of the molecule of interest. The recombinant fusion protein is  
 CC useful for detecting binding of a molecule of interest. The recombinant  
 CC fusion protein eliminates the need to construct two or more chimeric  
 CC proteins and enables the monitoring of biochemical events in live, intact  
 CC or fixed cells. The present sequence is used in the exemplification of  
 CC the present invention.  
 CC  
 SQ Sequence 7 AA;  
 XX  
 Query Match 100.0%; Score 41; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 1 RRMKMKK 7

RESULT 13  
 AA83577  
 ID AAY83577 standard; peptide; 8 AA.  
 XX  
 AC AAY83577;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Peptide fragment of penetratin.

XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.  
 XX  
 OS Synthetic.  
 XX WO200029427-A2.  
 XX PD 25-MAY-2000.  
 XX PF 11-NOV-1999; 99WO-GB003750.  
 XX PR 13-NOV-1998; 98GB-00025000.  
 XX PR 13-NOV-1998; 98GB-00025001.  
 XX PR 04-FEB-1999; 99GB-00002522.  
 XX PR 04-FEB-1999; 99GB-00002525.  
 XX PR 22-JUN-1999; 99GB-00014578.  
 XX PA (CYCL-) CYCLACEI LTD.  
 XX PI Fischer MP, Znelev N;  
 XX DR WPI; 2000-387734/33.  
 XX PT New membrane translocation peptide carrier group for delivering  
 PT therapeutic agents into target cells comprises specified sequence of  
 PT amino acids.  
 XX  
 XX Example 17; Page 44; 59pp; English.  
 XX  
 CC Penetratin is a membrane translocation polypeptide and as such, active  
 CC peptide fragments of penetratin can be used to translocate conjugated  
 CC molecules across the cell membrane e.g. drugs. 13 chemical entities are  
 CC described for use in the method such as pacitaxel.  
 CC 2'-succinimidopropionyl-Chetaa-RRMKKK-NH<sub>2</sub> 2. The method has applications as  
 CC succinimidopropionyl-Chetaa-RRMKKK-NH<sub>2</sub> 2. The method has applications as  
 CC a drug delivery system for treatment and therapy. The resulting  
 CC conjugated molecules exhibit high immunogenicity, solubility and  
 CC clearance. The penetratin peptide fragment may be truncated and or have  
 CC amino acid substitutions. See GENESBQ records AAY83520-Y83581  
 CC  
 SQ Sequence 8 AA;  
 XX  
 Query Match 100.0%; Score 41; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
 |||||  
 Db 2 RRMKMKK 8

RESULT 14  
 AAY83541  
 ID AAY83541 standard; peptide; 8 AA.  
 XX  
 AC AAY83541;  
 XX  
 DT 29-AUG-2000 (first entry)  
 XX  
 DE Peptide fragment of membrane transport vector penetratin.  
 XX  
 KW Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.  
 XX  
 OS Synthetic.  
 XX WO200029427-A2.  
 XX PD 25-MAY-2000.  
 XX PF 11-NOV-1999; 99WO-GB003750.  
 XX

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PR 13-NOV-1998; 98GB-00025000.
PR 13-NOV-1998; 98GB-00025001.
PR 04-FEB-1999; 99GB-00002522.
PR 04-FEB-1999; 99GB-00002525.
PR 22-JUN-1999; 99GB-00014578.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Fischer MP, Zhelev N;
XX
XX WPI; 2000-387734/33.
XX
XX New membrane translocation peptide carrier group for delivering
XX therapeutic agents into target cells comprises specified sequence of
XX amino acids.
XX
XX Claim 5; Page 26; 59pp; English.
XX
XX Penetratin is a membrane translocation polypeptide and as such, active
XX peptide fragments of penetratin can be used to translocate conjugated
XX molecules across the cell membrane e.g. drugs. 13 chemical entities are
XX described for use in the method such as paclitaxel.
XX
XX 2'succinimidopropionoyl-CbetaA-RRMKWK-NH-2, and podophyllotoxin-4-
XX
XX a drug delivery system for treatment and therapy. The resulting
XX conjugated molecules exhibit high immunogenicity, solubility and
XX clearance. The penetratin peptide fragment may be truncated and or have
XX amino acid substitutions. See GENSEQ records AAY83520-Y83581
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 41; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMKWK 7
Db 2 RRMKWK 8
RESULT 15
AAY83538
ID AAY83538 standard; peptide; 8 AA.
XX
XX AAY83538;
AC
XX
XX 29-AUG-2000 (first entry)
DT
XX
XX Peptide fragment of membrane transport vector penetratin.
DE
XX
XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;
XX conjugate; vector.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
XX FT 1 /label= Beta-alanine
XX FT /note= "Biotinylated"
XX
XX WO200029427-A2.
XX
XX 25-MAY-2000.
XX
XX 11-NOV-1999; 99WO-GB003750.
XX
XX 13-NOV-1998; 98GB-00025000.
XX 13-NOV-1998; 98GB-00025001.
XX 04-FEB-1999; 99GB-00002522.
XX 04-FEB-1999; 99GB-00002525.
XX 22-JUN-1999; 99GB-00014578.
XX
XX (CYCL-) CYCLACEL LTD.
PA

```

```

XX
XX Fischer MP, Zhelev N;
XX
XX WPI; 2000-387734/33.
XX
XX New membrane translocation peptide carrier group for delivering
XX therapeutic agents into target cells comprises specified sequence of
XX amino acids.
XX
XX Claim 1; Page 21; 59pp; English.
XX
XX Penetratin is a membrane translocation polypeptide and as such, active
XX peptide fragments of penetratin can be used to translocate conjugated
XX molecules across the cell membrane e.g. drugs. 13 chemical entities are
XX described for use in the method such as paclitaxel.
XX
XX 2'succinimidopropionoyl-CbetaA-RRMKWK-NH-2, and podophyllotoxin-4-
XX
XX a drug delivery system for treatment and therapy. The resulting
XX conjugated molecules exhibit high immunogenicity, solubility and
XX clearance. The penetratin peptide fragment may be truncated and or have
XX amino acid substitutions. See GENSEQ records AAY83520-Y83581
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 41; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RRMKWK 7
Db 2 RRMKWK 8

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Search completed: August 11, 2004, 14:00:37  
Job time : 54 secs



**Page 1**

| Result No. | Score | Query Match | Length | DB | ID                 | Description         |
|------------|-------|-------------|--------|----|--------------------|---------------------|
| 1          | 41    | 100.0       | 7      | 9  | US-09-854-204-2    | Sequence 2, Appli   |
| 2          | 41    | 100.0       | 7      | 9  | US-09-785-802A-6   | Sequence 6, Appli   |
| 3          | 41    | 100.0       | 7      | 10 | US-09-847-946A-123 | Sequence 123, App   |
| 4          | 41    | 100.0       | 7      | 10 | US-09-847-946A-130 | Sequence 130, App   |
| 5          | 41    | 100.0       | 7      | 12 | US-10-144-549-4    | Sequence 4, Appli   |
| 6          | 41    | 100.0       | 7      | 14 | US-10-229-915-11   | Sequence 11, Appli  |
| 7          | 41    | 100.0       | 7      | 14 | US-10-211-088-179  | Sequence 179, Appli |
| 8          | 41    | 100.0       | 7      | 14 | US-10-210-660-2    | Sequence 2, Appli   |
| 9          | 41    | 100.0       | 7      | 14 | US-10-210-660-26   | Sequence 26, Appli  |
| 10         | 41    | 100.0       | 7      | 14 | US-10-315-990-32   | Sequence 22, Appli  |
| 11         | 41    | 100.0       | 8      | 9  | US-09-854-204-5    | Sequence 6, Appli   |
| 12         | 41    | 100.0       | 8      | 9  | US-09-854-204-54   | Sequence 54, Appli  |
| 13         | 41    | 100.0       | 8      | 14 | US-10-229-915-10   | Sequence 10, App    |
| 14         | 41    | 100.0       | 8      | 14 | US-10-210-660-3    | Sequence 3, Appli   |
| 15         | 41    | 100.0       | 8      | 14 | US-10-210-660-34   | Sequence 24, Appli  |

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| 16 | 41 | 100.0 | 9  | US-09-854-204-7    | Sequence 7, Appl1   |
| 17 | 41 | 100.0 | 9  | US-09-854-204-53   | Sequence 53, Appl1  |
| 18 | 41 | 100.0 | 9  | US-09-854-204-61   | Sequence 61, Appl1  |
| 19 | 41 | 100.0 | 9  | US-09-854-204-62   | Sequence 62, Appl1  |
| 20 | 41 | 100.0 | 9  | US-10-228-915-9    | Sequence 9, Appl1   |
| 21 | 41 | 100.0 | 9  | US-10-210-660-4    | Sequence 4, Appl1   |
| 22 | 41 | 100.0 | 9  | US-10-210-660-19   | Sequence 19, Appl1  |
| 23 | 41 | 100.0 | 9  | US-10-210-660-21   | Sequence 21, Appl1  |
| 24 | 41 | 100.0 | 10 | US-09-854-204-8    | Sequence 8, Appl1   |
| 25 | 41 | 100.0 | 10 | US-09-854-204-52   | Sequence 52, Appl1  |
| 26 | 41 | 100.0 | 10 | US-10-228-915-8    | Sequence 8, Appl1   |
| 27 | 41 | 100.0 | 10 | US-10-210-660-5    | Sequence 5, Appl1   |
| 28 | 41 | 100.0 | 11 | US-09-854-204-51   | Sequence 51, Appl1  |
| 29 | 41 | 100.0 | 11 | US-10-228-915-7    | Sequence 7, Appl1   |
| 30 | 41 | 100.0 | 12 | US-09-854-204-50   | Sequence 50, Appl1  |
| 31 | 41 | 100.0 | 12 | US-09-847-966A-43  | Sequence 43, Appl1  |
| 32 | 41 | 100.0 | 12 | US-10-228-915-6    | Sequence 6, Appl1   |
| 33 | 41 | 100.0 | 13 | US-09-854-204-45   | Sequence 45, Appl1  |
| 34 | 41 | 100.0 | 13 | US-09-847-966A-143 | Sequence 143, Appl1 |
| 35 | 41 | 100.0 | 13 | US-10-228-915-10   | Sequence 10, Appl1  |
| 36 | 41 | 100.0 | 13 | US-10-097-175-102  | Sequence 102, Appl1 |
| 37 | 41 | 100.0 | 13 | US-10-228-915-5    | Sequence 5, Appl1   |
| 38 | 41 | 100.0 | 14 | US-09-854-204-48   | Sequence 48, Appl1  |
| 39 | 41 | 100.0 | 14 | US-10-228-915-4    | Sequence 4, Appl1   |
| 40 | 41 | 100.0 | 15 | US-09-854-204-47   | Sequence 47, Appl1  |
| 41 | 41 | 100.0 | 15 | US-09-865-281-18   | Sequence 18, Appl1  |
| 42 | 41 | 100.0 | 15 | US-10-228-915-3    | Sequence 3, Appl1   |
| 43 | 41 | 100.0 | 16 | US-08-610-220A-9   | Sequence 9, Appl1   |
| 44 | 41 | 100.0 | 16 | US-09-814-371-43   | Sequence 43, Appl1  |
| 45 | 41 | 100.0 | 16 | US-09-780-070-38   | Sequence 38, Appl1  |

## ALIGNMENTS

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RESULT 1
US-09-854-204-2
Sequence 2, Application US/09654204
Patent No. US20020096236A1
GENERAL INFORMATION:
APPLICANT: Fischer, Peter Martin
APPLICANT: Zhelev, Nikolai
TITLE OF INVENTION: Transport Vectors
FILE REFERENCE: CCI-010
CURRENT APPLICATION NUMBER: US/09/854,204
PRIORITY FILING DATE: 2001-05-11
PRIORITY FILING DATE: 1999-11-12
PRIORITY FILING DATE: 1999-11-12
PRIORITY FILING DATE: 1998-11-13
PRIORITY FILING DATE: 1998-11-13
PRIORITY FILING DATE: 1998-11-13
PRIORITY FILING DATE: 1999-02-04
PRIORITY FILING DATE: 1999-02-04
PRIORITY FILING DATE: 1999-07-04
PRIORITY FILING DATE: 1999-06-22
PRIORITY FILING DATE: 1999-11-11
PRIORITY FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: sequence
NAME/KEY: MOD_RRS
LOCATION: (7)
OTHER INFORMATION: Amidation, the carboxy terminal lysine residue may
OTHER INFORMATION: have its carboxyl group converted into an

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OTHER INFORMATION: carbosamide group.  
US-09-854-204-2

Query Match 100.0%; Score 41; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 2  
US-09-785-802A-6

Sequence 6, Application US/09785802A  
Patent No. US20020151004A1

GENERAL INFORMATION:

APPLICANT: Craig, Roger

TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME

FILE REFERENCE: 11067/2035

CURRENT APPLICATION NUMBER: US/09/785,802A

CURRENT FILING DATE: 2001-02-16

PRIOR APPLICATION NUMBER: US 09/748,06

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/748,789

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 6

LENGTH: 7

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-785-802A-6

Query Match

Best Local Similarity 100.0%; Score 41; DB 9; Length 7;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 3  
US-09-847-946A-123

Sequence 123, Application US/09847946A

Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 123

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: Description of Artificial Sequence:membrane

OTHER INFORMATION: translocation domain

US-09-847-946A-123

Query Match 100.0%; Score 41; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 4  
US-09-847-946A-130

Sequence 130, Application US/09847946A  
Publication No. US20030054999A1

GENERAL INFORMATION:

APPLICANT: May, Michael J

APPLICANT: Ghosh, Sankar

APPLICANT: Findeis, Mark A

APPLICANT: Phillips, Kathryn

TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF

FILE REFERENCE: PPI-119

CURRENT APPLICATION NUMBER: US/09/847,946A

CURRENT FILING DATE: 2001-05-02

PRIOR APPLICATION NUMBER: 60/201,261

PRIOR FILING DATE: 2000-05-02

PRIOR APPLICATION NUMBER: 09/643,260

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 160

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 130

LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:membrane

US-09-847-946A-130

Query Match 100.0%; Score 41; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 5  
US-10-144-549-4

Sequence 4, Application US/10144549

Publication No. US20030211590A1

GENERAL INFORMATION:

APPLICANT: Geneshuttle Biopharm, Inc.

APPLICANT: Hwu, Paul L.

TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR

FILE REFERENCE: MBHB 02-340

CURRENT APPLICATION NUMBER: US/10/144,549

CURRENT FILING DATE: 2002-05-13

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 4

LENGTH: 7

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-10-144-549-4

Query Match 100.0%; Score 41; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

## RESULT 6

US-10-229-915-11  
; Sequence 11, Application US/10229915  
; Publication No. US20030083262A1  
; GENERAL INFORMATION:  
; APPLICANT: Lazarus, Douglas  
; APPLICANT: Hanig, Gerhard  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY  
; FILE REFERENCE: PPI-127  
; CURRENT APPLICATION NUMBER: US/10/229,915  
; PRIOR FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: US 60/316,328  
; PRIOR FILING DATE: 2001-08-30  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: anti-inflammatory compound  
US-10-229-915-11

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
| | | | |  
Db 1 RRMKWK 7

## RESULT 7

US-10-211-088-179  
; Sequence 179, Application US/10211088  
; Publication No. US20030104479A1  
; GENERAL INFORMATION:  
; APPLICANT: Bright, Gary R.  
; APPLICANT: Premkumar, D. David  
; APPLICANT: Chem, Yih-Tai  
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular Bi  
; FILE REFERENCE: 01-1022-US  
; CURRENT APPLICATION NUMBER: US/10/211,088  
; CURRENT FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: 60/309,395  
; PRIOR FILING DATE: 2001-08-01  
; PRIOR APPLICATION NUMBER: 60/341,589  
; PRIOR FILING DATE: 2001-12-13  
; NUMBER OF SEQ ID NOS: 366  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 179  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Nuclear localization signal  
US-10-211-088-179

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
| | | | |  
Db 1 RRMKWK 7

## RESULT 8

US-10-210-660-2  
; Sequence 2, Application US/10210660  
; Publication No. US20030119735A1

## GENERAL INFORMATION:

; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/10/210,660  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US/09/346,847  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-2

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
| | | | |  
Db 1 RRMKWK 7

## RESULT 9

US-10-210-660-26  
; Sequence 26, Application US/10210660  
; Publication No. US20030119735A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, M. Peter  
; APPLICANT: Wang, Shudong  
; TITLE OF INVENTION: Delivery System  
; FILE REFERENCE: CCI-009  
; CURRENT APPLICATION NUMBER: US/10/210,660  
; CURRENT FILING DATE: 2002-07-31  
; PRIOR APPLICATION NUMBER: US/09/346,847  
; PRIOR FILING DATE: 1999-07-02  
; PRIOR APPLICATION NUMBER: GB 9814527  
; PRIOR FILING DATE: 1998-07-03  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (7)\_"RES  
; OTHER INFORMATION: AMIDATION  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-26

## Query Match

100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
| | | | |  
Db 1 RRMKWK 7

## RESULT 10

US-10-315-920-22  
; Sequence 22, Application US/10315920

```
Publication No. US20030175809A1
GENERAL INFORMATION:
APPLICANT: Fradkov, Arcady Fedorovich
APPLICANT: Terzikikh, Alexey
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS
FILE REFERENCE: CION-077CIP
CURRENT APPLICATION NUMBER: US/10/315,920
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: 60/211,607
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: PCT/US01/19097
PRIOR FILING DATE: 2001-06-13
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nuclear localization signal
US-10-315-920-22

Query Match      100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 1 RRMKKKK 7

RESULT 11
US-09-854-204-6
Sequence 6, Application US/09854204
Patent No. US20020098236A1
GENERAL INFORMATION:
APPLICANT: Fischer, Peter Martin
APPLICANT: Zhelev, Nikolai
TITLE OF INVENTION: Transport Vectors
FILE REFERENCE: CCI-010
CURRENT APPLICATION NUMBER: US/09/854,204
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/438,460
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: GB 9825000.4
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9825001.2
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9902525.6
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9902522.3
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9914578.1
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/GB99/03750
PRIOR FILING DATE: 1999-11-11
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-854-204-6

Query Match      100.0%; Score 41; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 1 RRMKKKK 7
```

```
Db 2 RRMKKKK 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Data
LOCATION: (8)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-854-204-54

Query Match      100.0%; Score 41; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 2 RRMKKKK 8

RESULT 12
US-09-854-204-54
Sequence 54, Application US/09854204
Patent No. US20020098236A1
GENERAL INFORMATION:
APPLICANT: Fischer, Peter Martin
APPLICANT: Zhelev, Nikolai
TITLE OF INVENTION: Transport Vectors
FILE REFERENCE: CCI-010
CURRENT APPLICATION NUMBER: US/09/854,204
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/438,460
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: GB 9825000.4
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9825001.2
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: GB 9902525.6
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9902522.3
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: GB 9914578.1
PRIOR FILING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: PCT/GB99/03750
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 54
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Data
LOCATION: (8)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-229-915-10

Query Match      100.0%; Score 41; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 2 RRMKKKK 8

RESULT 13
US-10-229-915-10
Sequence 10, Application US/10229915
Patent No. US20030083262A1
GENERAL INFORMATION:
APPLICANT: Lazarus, Douglas
APPLICANT: Hannig, Gerhard
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
FILE REFERENCE: PPI-127
CURRENT APPLICATION NUMBER: US/10/229,915
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: US 60/316,328
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 8
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Wed Aug 11 15:42:13 2004

us-09-854-204-2.open.rapb

Page 5

TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: anti-inflammatory compound  
US-10-229-915-10

Query Match 100.0%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 2 RRMKWK 8

RESULT 14  
US-10-210-660-3  
Sequence 3, Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-3

Query Match 100.0%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 2 RRMKWK 8

RESULT 15  
US-10-210-660-24  
Sequence 24, Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 8  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
NAME/KEY: MOD\_RES

LOCATION: (1)  
OTHER INFORMATION: bala  
FEATURE:  
NAME/KEY: MOD\_RES  
LOCATION: (8)  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
FEATURE:  
OTHER INFORMATION: AMIDATION  
US-10-210-660-24

Query Match 100.0%; Score 41; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
Db 2 RRMKWK 8

Search completed: August 11, 2004, 14:07:20  
Job time : 42 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 11, 2004, 13:59:42 ; Search time 18 Seconds  
(without alignments)  
20.077 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1 RRMKMK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/6C.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/6D.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Query Length | DB ID             | Description        |
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| 2          | 41    | 100.0 | 7            | US-09-346-847-26  | Sequence 26, Appli |
| 3          | 41    | 100.0 | 8            | US-09-346-847-3   | Sequence 3, Appli  |
| 4          | 41    | 100.0 | 8            | US-09-346-847-24  | Sequence 24, Appli |
| 5          | 41    | 100.0 | 9            | US-09-346-847-4   | Sequence 4, Appli  |
| 6          | 41    | 100.0 | 9            | US-09-346-847-19  | Sequence 19, Appli |
| 7          | 41    | 100.0 | 9            | US-09-346-847-21  | Sequence 21, Appli |
| 8          | 41    | 100.0 | 10           | US-09-346-847-5   | Sequence 5, Appli  |
| 9          | 41    | 100.0 | 16           | US-08-928-958-7   | Sequence 7, Appli  |
| 10         | 41    | 100.0 | 16           | US-08-810-540-3   | Sequence 3, Appli  |
| 11         | 41    | 100.0 | 16           | US-08-810-540-6   | Sequence 6, Appli  |
| 12         | 41    | 100.0 | 16           | US-09-072-429-7   | Sequence 7, Appli  |
| 13         | 41    | 100.0 | 16           | US-08-964-302A-6  | Sequence 6, Appli  |
| 14         | 41    | 100.0 | 16           | US-09-116-294-4   | Sequence 4, Appli  |
| 15         | 41    | 100.0 | 16           | US-08-964-614A-4  | Sequence 4, Appli  |
| 16         | 41    | 100.0 | 16           | US-08-849-486-1   | Sequence 1, Appli  |
| 17         | 41    | 100.0 | 16           | US-08-849-486-4   | Sequence 4, Appli  |
| 18         | 41    | 100.0 | 16           | US-08-849-486-5   | Sequence 5, Appli  |
| 19         | 41    | 100.0 | 16           | US-09-208-966-1   | Sequence 1, Appli  |
| 20         | 41    | 100.0 | 16           | US-09-208-966-54  | Sequence 54, Appli |
| 21         | 41    | 100.0 | 16           | US-09-308-935-8   | Sequence 8, Appli  |
| 22         | 41    | 100.0 | 16           | US-09-441-416A-6  | Sequence 6, Appli  |
| 23         | 41    | 100.0 | 16           | US-09-296-089-33  | Sequence 33, Appli |
| 24         | 41    | 100.0 | 16           | US-09-419-826-35  | Sequence 35, Appli |
| 25         | 41    | 100.0 | 16           | US-09-466-772-7   | Sequence 7, Appli  |
| 26         | 41    | 100.0 | 16           | US-09-302-305C-10 | Sequence 10, Appli |
| 27         | 41    | 100.0 | 16           | US-09-402-929-7   | Sequence 7, Appli  |

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| 29 | 41 | 100.0 | 16 | US-09-346-847-25  | Sequence 25, Appli |
| 30 | 41 | 100.0 | 16 | US-09-057-363C-47 | Sequence 47, Appli |
| 31 | 41 | 100.0 | 16 | US-09-043-560B-3  | Sequence 3, Appli  |
| 32 | 41 | 100.0 | 16 | US-09-648-400A-29 | Sequence 29, Appli |
| 33 | 41 | 100.0 | 16 | US-09-227-652B-4  | Sequence 4, Appli  |
| 34 | 41 | 100.0 | 16 | US-09-780-070-38  | Sequence 38, Appli |
| 35 | 41 | 100.0 | 16 | US-08-610-220B-9  | Sequence 9, Appli  |
| 36 | 41 | 100.0 | 16 | US-09-775-052A-1  | Sequence 1, Appli  |
| 37 | 41 | 100.0 | 16 | US-09-775-052A-34 | Sequence 54, Appli |
| 38 | 41 | 100.0 | 16 | US-09-155-165-22  | Sequence 22, Appli |
| 39 | 41 | 100.0 | 16 | US-09-792-480-29  | Sequence 29, Appli |
| 40 | 41 | 100.0 | 16 | US-09-792-480-30  | Sequence 30, Appli |
| 41 | 41 | 100.0 | 16 | US-09-551-976-33  | Sequence 33, Appli |
| 42 | 41 | 100.0 | 16 | US-09-265-107-47  | Sequence 47, Appli |
| 43 | 41 | 100.0 | 17 | US-09-346-847-17  | Sequence 17, Appli |
| 44 | 41 | 100.0 | 17 | US-09-346-847-20  | Sequence 20, Appli |
| 45 | 41 | 100.0 | 17 | US-09-346-847-22  | Sequence 22, Appli |

#### ALIGNMENTS

RESULT 1  
US-09-346-847-2  
Sequence 2, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-346-847-2

Query Match 100.0%; Score 41; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 38+05;  
Matches 7; Conservative 0; Mismatches 0; Gaps 0;  
QY 1 RRMKMK 7  
Db 1 RRMKMK 7  
RESULT 2  
US-09-346-847-26  
Sequence 26, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 26  
LENGTH: 7

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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)
OTHER INFORMATION: AMIDATION
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-346-847-26
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Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy
1 RRMKWKX 7
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Db
1 RRMKWKX 7
```

```
RESULT 3
US-09-346-847-3
Sequence 3, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-346-847-3
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Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy
1 RRMKWKX 7
|||||
Db
2 RRMKWKX 8
```

```
RESULT 4
US-09-346-847-24
Sequence 24, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
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LOCATION: (1)
OTHER INFORMATION: bala
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: AMIDATION
US-09-346-847-24
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```
Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy
1 RRMKWKX 7
|||||
Db
2 RRMKWKX 8
```

```
RESULT 5
US-09-346-847-4
Sequence 4, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-346-847-4
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```
Query Match
Best Local Similarity 100.0%; Score 41; DB 4; Length 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy
1 RRMKWKX 7
|||||
Db
3 RRMKWKX 9
```

```
RESULT 6
US-09-346-847-19
Sequence 19, Application US/09346847
Patent No. 6472507
GENERAL INFORMATION:
APPLICANT: Fischer, M. Peter
APPLICANT: Wang, Shudong
TITLE OF INVENTION: Delivery System
FILE REFERENCE: CCI-009
CURRENT APPLICATION NUMBER: US/09/346,847
CURRENT FILING DATE: 1999-07-02
PRIOR APPLICATION NUMBER: GB 9814527
PRIOR FILING DATE: 1998-07-03
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (2)
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OTHER INFORMATION: bala  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
NAME/KEY: MOD\_RES  
LOCATION: (9)  
OTHER INFORMATION: AMIDATION  
US-09-346-847-19

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
|||  
Db 3 RRMKMK 9

RESULT 7  
US-09-346-847-21  
Sequence 21, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
APPLICANT: Wang, Shudong  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 21  
LENGTH: 9  
TYPE: PRP  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
NAME/KEY: MOD\_RES  
LOCATION: (9)  
OTHER INFORMATION: AMIDATION  
US-09-346-847-21

Query Match 100.0%; Score 41; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
|||  
Db 2 RRMKMK 8

RESULT 8  
US-09-346-847-5  
Sequence 5, Application US/09346847  
Patent No. 6472507  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
APPLICANT: Wang, Shudong  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/09/346,847  
CURRENT FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 10  
TYPE: PRP  
ORGANISM: Artificial Sequence  
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: peptide  
US-09-346-847-5

Query Match 100.0%; Score 41; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.82;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
|||  
Db 4 RRMKMK 10

RESULT 9  
US-08-928-958-7  
Sequence 7, Application US/08928958  
Patent No. 5877282  
GENERAL INFORMATION:  
APPLICANT: NADLER, STEVEN G.  
APPLICANT: CLEARLAND, JEFFREY S.  
APPLICANT: BLAKE, JAMES  
APPLICANT: HAPPAR, OMAR K.  
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN  
TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND  
TITLE OF INVENTION: METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBINS & ASSOCIATES  
STREET: 90 MIDDLEFIELD ROAD, SUITE 200  
CITY: MENLO PARK  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/928,958  
FILING DATE: 12-SEP-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/026978  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINS, ROBERTA L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5998-0019  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 325-7812  
TELEFAX: (650) 325-7823  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-928-958-7

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
|||  
Db 10 RRMKMK 16

RESULT 10  
US-08-810-540-3  
Sequence 3, Application US/08810540

Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
APPLICANT: Shelanski, Michael L.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-3

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
DB 10 RRMKKK 16

RESULT 11  
US-08-810-540-6  
Sequence 6, Application US/08810540  
Patent No. 5929042  
GENERAL INFORMATION:  
APPLICANT: Troy, Carol M.  
APPLICANT: Shelanski, Michael L.  
TITLE OF INVENTION: ANTISENSE COMPOUNDS WHICH PREVENT CELL  
TITLE OF INVENTION: DEATH AND USES THEREOF  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham, LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/810,540  
FILING DATE: 03-MAR-1997

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: White Esq., John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51247  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0526  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-810-540-6

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
DB 10 RRMKKK 16

RESULT 12  
US-09-072-429-7  
Sequence 7, Application US/09072429  
Patent No. 5962415  
GENERAL INFORMATION:  
APPLICANT: Nadler, Steven G.  
TITLE OF INVENTION: COMPOSITIONS COMPRISING A PEPTIDE  
TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLLOCATION AND AN  
TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Bristol-Myers Squibb Company  
STREET: P.O. Box 4000  
CITY: Princeton  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08543-4000  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,429  
FILING DATE: 04-MAY-1998  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Klein, Christopher A.  
REGISTRATION NUMBER: 34,363  
REFERENCE/DOCKET NUMBER: 090141b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (609) 252-3714  
TELEFAX: (609) 252-4526  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 16 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-072-429-7

Query Match 100.0%; Score 41; DB 2; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7

Db 10 RRMKWK 16

## RESULT 13

US-08-964-302A-6  
Sequence 6, Application US/08964302A

Patent No. 6015787

GENERAL INFORMATION:

APPLICANT: Potter, David A.

TITLE OF INVENTION: CELL-PERMEABLE PROTEIN INHIBITORS OF CALPAIN

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,302A

FILING DATE: 04-NOV-1997

ATTORNEY/AGENT INFORMATION:

NAME: Melkielejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-964-302A-6

Query Match

Best Local Similarity 100.0%; Score 41; DB 3; Length 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7

Db 10 RRMKWK 16

RESULT 14

US-09-116-294-4

Sequence 4, Application US/09116294

Patent No. 6025140

GENERAL INFORMATION:

APPLICANT: Langel, Ulo

APPLICANT: Bartfai, Tamas

APPLICANT: Pooza, Margus

APPLICANT: Valkna, Andres

APPLICANT: Saar, Kulliki

TITLE OF INVENTION: Conjugated Constructs of Peptides and

TITLE OF INVENTION: Nucleic Acid Analogs, and Their Transport Across Membranes

FILE REFERENCE: 4394

CURRENT APPLICATION NUMBER: US/09/116,294

CURRENT FILING DATE: 1998-07-16

EARLIER APPLICATION NUMBER: 60/052,678

EARLIER FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4  
LENGTH: 16  
TYPE: PRT  
ORGANISM: drosophila  
US-09-116-294-4

## Query Match

Best Local Similarity 100.0%; Score 41; DB 3; Length 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7

Db 10 RRMKWK 16

## RESULT 15

US-08-964-614A-4

Sequence 4, Application US/08964614A

Patent No. 6057104

GENERAL INFORMATION:

APPLICANT: Hasely, Paul

TITLE OF INVENTION: DISRUPTION OF THE MAMMALIAN

TITLE OF INVENTION: Rad51 PROTEIN AND DISRUPTION OF PROTEINS THAT ASSOCIATE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds, LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036-2811

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows

SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,614A

FILING DATE: 05-NOV-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/758,280

FILING DATE: 05-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 8535-0019-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-493-4935

TELEFAX: 650-493-5556

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-964-614A-4

QY 1 RRMKWK 7

Db 10 RRMKWK 16

Query Match

Best Local Similarity 100.0%; Score 41; DB 3; Length 16;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7

Db 10 RRMKWK 16

Search completed: August 11, 2004, 14:02:44

Job time: 18 secs

***This Page Blank (uspto)***

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2004, 14:06:34 ; Search time 16 Seconds  
(without alignments)  
42.084 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*\*\*  
1: pir1:\*\*\*  
2: pir2:\*\*\*  
3: pir3:\*\*\*  
4: pir4:\*\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 17    | 41.5        | 7      | 2 S33244 | neuromodulatory pe  |
| 2          | 17    | 41.5        | 7      | 2 S33245 | neuromodulatory pe  |
| 3          | 16    | 39.0        | 3      | 3 F37196 | bradykinin-potent   |
| 4          | 16    | 39.0        | 5      | 2 UH0253 | gut pentapeptide    |
| 5          | 16    | 39.0        | 5      | 2 G37196 | bradykinin-potent   |
| 6          | 16    | 39.0        | 7      | 2 PN0649 | pullulanase (EC 3.  |
| 7          | 15    | 36.6        | 5      | 2 A60803 | neuropeptide - sea  |
| 8          | 15    | 36.6        | 6      | 2 I49424 | cytotoxic T-lympho  |
| 9          | 14    | 34.1        | 7      | 2 S33245 | neuromodulatory pe  |
| 10         | 14    | 34.1        | 6      | 4 I79564 | hypothetical TGL3   |
| 11         | 12    | 29.3        | 4      | 2 I40870 | phospholipase C (E  |
| 12         | 12    | 29.3        | 5      | 2 PT0308 | ig heavy chain CRD  |
| 13         | 12    | 29.3        | 6      | 2 S66195 | alcohol dehydrogen  |
| 14         | 12    | 29.3        | 6      | 2 S11024 | hydrogensulfite re  |
| 15         | 12    | 29.3        | 6      | 2 S11556 | hydrogensulfite re  |
| 16         | 12    | 29.3        | 6      | 2 A31263 | dihydrofolate redu  |
| 17         | 12    | 29.3        | 6      | 2 B31263 | ceribellar degener  |
| 18         | 12    | 29.3        | 6      | 2 B3640  | ribosomal protein   |
| 19         | 12    | 29.3        | 7      | 2 S19630 | hypothetical pepti  |
| 20         | 11    | 26.8        | 4      | 2 A34662 | RPCH-related neuro  |
| 21         | 11    | 26.8        | 4      | 2 B53284 | T-cell receptor be  |
| 22         | 11    | 26.8        | 4      | 2 PT0661 | T-cell receptor be  |
| 23         | 11    | 26.8        | 4      | 2 A32516 | cholecystokinin-5   |
| 24         | 11    | 26.8        | 5      | 2 PT0281 | ig heavy chain CRD  |
| 25         | 11    | 26.8        | 5      | 2 PT0729 | T-cell receptor be  |
| 26         | 11    | 26.8        | 5      | 2 PT0560 | T-cell receptor be  |
| 27         | 11    | 26.8        | 6      | 2 B34835 | dnaa protein - pse  |
| 28         | 11    | 26.8        | 6      | 2 A61068 | locustactinin - mlg |
| 29         | 11    | 26.8        | 6      | 2 A61068 | locustactinin - mlg |

|    |    |      |   |          |                    |
|----|----|------|---|----------|--------------------|
| 30 | 11 | 26.8 | 6 | 2 PT0629 | T-cell receptor be |
| 31 | 11 | 26.8 | 6 | 2 PT0532 | T-cell receptor be |
| 32 | 11 | 26.8 | 6 | 2 PT0519 | T-cell receptor be |
| 33 | 11 | 26.8 | 6 | 2 PT0637 | T-cell receptor be |
| 34 | 11 | 26.8 | 6 | 2 PT0641 | T-cell receptor be |
| 35 | 11 | 26.8 | 6 | 2 PT0726 | T-cell receptor be |
| 36 | 11 | 26.8 | 6 | 2 F41946 | T-cell receptor ga |
| 37 | 11 | 26.8 | 6 | 2 PD0028 | pev-kinin 2 - pena |
| 38 | 11 | 26.8 | 7 | 2 S21230 | demorphin (Trp-4,  |
| 39 | 11 | 26.8 | 7 | 2 A58512 | venom heptapeptide |
| 40 | 11 | 26.8 | 7 | 2 A61081 | cryptophyllin, bas |
| 41 | 11 | 26.8 | 7 | 2 S57274 | triacylglycerol 11 |
| 42 | 11 | 26.8 | 7 | 2 S09652 | hypothetical prote |
| 43 | 11 | 26.8 | 7 | 2 PQ0727 | H2 class I protein |
| 44 | 11 | 26.8 | 7 | 2 E48394 | glycoprotein compo |
| 45 | 11 | 26.8 | 7 | 2 B33541 | hypothetical prote |

## ALIGNMENTS

RESULT 1  
S33244  
neuromodulatory peptide Wamide-1 - giant African snail  
C:Species: Achatina fulica (giant African snail)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S33244  
R:Minakata, H.; Ikeda, T.; Munoeke, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 323: 104-108, 1993  
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t  
A:Reference number: S33244; MUID:93265912; PMID:8495720  
A:Accession: S33244  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MIN>

Query Match 41.5%; Score 17; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKK 7  
DB 1 WKE 3

RESULT 2  
S33246  
neuromodulatory peptide Wamide-3 - giant African snail  
C:Species: Achatina fulica (giant African snail)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S33246  
R:Minakata, H.; Ikeda, T.; Munoeke, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 323: 104-108, 1993  
A:Title: Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of t  
A:Reference number: S33244; MUID:93265912; PMID:8495720  
A:Accession: S33246  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MIN>

Query Match 41.5%; Score 17; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKK 7  
DB 1 WKO 3

RESULT 3  
F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C:Species: Bothrops insularis (island jararaca)



OY 1 RMK 4  
1 RMK 4

## RESULT 9

S33245  
neuromodulatory peptide Wamide-2 - giant African snail  
C:Species: Achatina fulica (giant African snail)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C/Accession: S33245  
R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.  
FEBS Lett. 323, 104-108, 1993  
A>Title: Wamide-1, -2 and -3; novel neuromodulatory peptides isolated from ganglia of  
A:Reference number: S33244; MUID:93265912; PMID:8495720  
A:Accession: S33245  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MIN>

Query Match 34.1%; Score 14; DB 2; Length 7;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 WK 7  
1 WRE 3

## RESULT 10

I79564  
hypothetical TCU3 protein (mitochondrial) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 28-Jan-2000 #sequence\_revision 28-Jan-2000 #text\_change 28-Jan-2000  
C/Accession: I79564  
R:Butter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;  
Proc Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990  
A>Title: The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del  
A:Reference number: I59162; MUID:90222189; PMID:2326274  
A:Accession: I79564  
A>Status: translation not shown; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <ZUN>  
A:Cross-references: GB:M33602; NID:9339907; PIDN:AA66449.1; PID:9807656  
C:Comment: This is the hypothetical translation of a sequence translated in an incorrect

Query Match 31.7%; Score 13; DB 4; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 KM 5  
1 RW 2

## RESULT 11

I40870  
phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)  
C:Species: Clostridium perfringens  
C>Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 21-Jul-2000  
C/Accession: I40870  
R:Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.  
Microbiol. Immunol. 36, 603-613, 1992  
A>Title: Role of the upstream region containing an intrinsic DNA curvature in the negati  
A:Reference number: I40870; MUID:92396045; PMID:1522810  
A:Accession: I40870  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-4 <RES>  
A:Cross-references: EMBL:X62825; NID:940622; PIDN:CAA44636.1; PID:94377417  
C:Genetics:  
A:Gene: plc

C:Keywords: phosphoric diester hydrolase

Query Match 29.3%; Score 12; DB 2; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 MKK 6  
1 MKK 4

## RESULT 12

PT0308  
IG heavy chain CRD3 region (clone 6-88) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C/Accession: PT0308  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A:Reference number: PT0222; MUID:9108337; PMID:1899102  
A:Accession: PT0308  
A:Molecule type: DNA  
A:Residues: 1-5 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.3%; Score 12; DB 2; Length 5;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 WK 6  
2 WE 3

## RESULT 13

S66195  
alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragme  
C:Species: Gadus sp. (cod)  
C>Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998  
C/Accession: S66195  
R:Hjeltnyst, L.; Hackett, M.; Shafiq, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;  
FEBS Lett. 367, 237-240, 1995  
A>Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. N  
nzyme.  
A:Reference number: S66191; MUID:95331382; PMID:7607314  
A:Accession: S66195  
A:Molecule type: protein  
A:Residues: 1-6 <HJE>  
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
C:Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 29.3%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 WK 6  
5 WE 6

## RESULT 14

S11024  
hydroxynitrite reductase (EC 1.8.99.3) chain 1 - Desulfovibrio thermophilus (fragment)  
N:Alternate names: disulfite reductase; desulfotiscidin  
C:Species: Desulfovibrio thermophilus  
C>Date: 19-Mar-1997 #sequence\_revision 30-Jan-1998 #text\_change 30-Jan-1998  
C/Accession: S11024  
R:Paugue, G.; Lino, A.R.; Czochowski, M.; Kang, L.; DeVatraman, D.V.; Moura, J.J.G.; I  
Biochim. Biophys. Acta 1040, 112-118, 1990  
A>Title: Purification and characterization of bisulfite reductase (desulfotiscidin) from  
A:Reference number: S11024; MUID:90335276; PMID:2165817

A;Accession: S11024  
 A;Molecule type: protein  
 A;Residues: 1-6 <FAU>  
 C;Keywords: oxidoreductase

Query Match 29.3%; Score 12; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKWK 6  
 :|:|  
 Db 3 VKFK 6

## RESULT 15

S11556  
 hydrogensulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragment)  
 N;Alternate names: bisulfite reductase; desulfofuscidin  
 C;Species: Desulfovibrio thermophilus  
 C;Date: 19-Mar-1997 #sequence\_revision 12-Dec-1997 #text\_change 30-Jan-1998  
 C;Accession: S11556  
 R;Faure, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DeVartanian, D.V.; Moura, J.C.G.; I  
 Biochim. Biophys. Acta 1040, 112-118, 1990  
 A;Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from  
 A;Reference number: S11024; MUID:90335276; PMID:2165817  
 A;Accession: S11556  
 A;Molecule type: protein  
 A;Residues: 1-6 <FAU>  
 C;Keywords: oxidoreductase

Query Match 29.3%; Score 12; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KWK 6  
 :|:|  
 Db 4 KYK 6

Search completed: August 11, 2004, 14:09:58  
 Job time : 17 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 11, 2004, 14:02:48 ; Search time 13 Seconds

(without alignments)  
28,038 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41  
Sequence: 1 RRMKMK 7

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID         | Description         |
|------------|-------|-------------|--------|------------|---------------------|
| 1          | 17    | 41.5        | 7      | WMA2_ACHFU | P35920 achatina fu  |
| 2          | 17    | 41.5        | 7      | WMA3_ACHFU | P35921 achatina fu  |
| 3          | 16    | 39.0        | 5      | BPP7_BOTIN | P30425 bochrops fu  |
| 4          | 14    | 34.1        | 7      | WMA1_ACHFU | P35919 achatina fu  |
| 5          | 13    | 31.7        | 5      | UF01_MOUSE | P38633 mus musculus |
| 6          | 12    | 29.3        | 7      | Y151_LITRU | P82065 litorea rub  |
| 7          | 11    | 26.8        | 4      | OCP3_OCTMI | P58649 octopus min  |
| 8          | 11    | 26.8        | 6      | E101_LITRU | P82096 litorea rub  |
| 9          | 11    | 26.8        | 7      | LOK1_LOCOM | P41491 locusta mig  |
| 10         | 11    | 26.8        | 7      | BRHP_CONIM | P58803 conus imper  |
| 11         | 11    | 26.8        | 7      | TPRY_PACDA | P83455 pachymedusa  |
| 12         | 10    | 24.4        | 6      | VP19_HSVIK | P23210 herpes simp  |
| 13         | 8     | 19.5        | 4      | FAR4_HIRME | P45563 hitudo medi  |
| 14         | 8     | 19.5        | 4      | FMK7_MACNI | P01162 macrocallis  |
| 15         | 8     | 19.5        | 7      | FAR3_HABCO | P81298 haemochus    |
| 16         | 8     | 19.5        | 7      | FAR3_PANRE | P41874 panagrellus  |
| 17         | 8     | 19.5        | 7      | FARS_HIRME | P42564 hitudo medi  |
| 18         | 8     | 19.5        | 7      | FARB_CALVO | P41866 calliphora   |
| 19         | 7     | 17.1        | 5      | FARP_ARTTR | P41853 arthropochi  |
| 20         | 7     | 17.1        | 6      | ACPH_RABIT | P23154 oryctolagus  |
| 21         | 7     | 17.1        | 6      | OVN_LBEPD  | P42985 lepidolatus  |
| 22         | 7     | 17.1        | 7      | ALU7_CYDPO | P82158 cydia pomon  |
| 23         | 7     | 17.1        | 7      | CARP_MYTED | P10420 mytilus edu  |
| 24         | 7     | 17.1        | 7      | HV7_FIG    | P01153 sus scrofa   |
| 25         | 6     | 14.6        | 3      | LUXE_VIBRI | P24272 vibrio fisc  |
| 26         | 6     | 14.6        | 4      | FRFA_ATEL  | P58705 anhopleura   |
| 27         | 6     | 14.6        | 4      | FIRI_ATEL  | P58706 anhopleura   |
| 28         | 6     | 14.6        | 6      | ASP2_IACSN | P82655 lactobacill  |
| 29         | 5     | 12.2        | 3      | GRWM_HUMAN | P01157 homo sapien  |
| 30         | 5     | 12.2        | 4      | DCML_PSECH | P19191 pseudomonas  |
| 31         | 5     | 12.2        | 4      | DCMS_PSECH | P19198 pseudomonas  |
| 32         | 5     | 12.2        | 4      | FAR3_HIRME | P42564 hitudo medi  |
| 33         | 5     | 12.2        | 4      | FLRF_HIRME | P42561 hitudo medi  |

|    |   |      |   |   |            |                    |
|----|---|------|---|---|------------|--------------------|
| 34 | 5 | 12.2 | 4 | 1 | FLRN_ATEL  | P58707 anhopleura  |
| 35 | 5 | 12.2 | 4 | 1 | BIOA_CITFR | P01868 homo sapien |
| 36 | 5 | 12.2 | 5 | 1 | BIOB_CITFR | P13071 citrobacter |
| 37 | 5 | 12.2 | 5 | 1 | BIOB_CITFR | P12997 citrobacter |
| 38 | 5 | 12.2 | 5 | 1 | BIOB_CITFR | P82099 litorea rub |
| 39 | 5 | 12.2 | 5 | 1 | PRCT_PERAM | P13733 periplaneta |
| 40 | 5 | 12.2 | 5 | 1 | TRM3_ECOLI | P13973 escherichia |
| 41 | 5 | 12.2 | 6 | 1 | CIP1_MYTED | P13736 mytilus edu |
| 42 | 5 | 12.2 | 6 | 1 | CIP2_MYTED | P13737 mytilus edu |
| 43 | 5 | 12.2 | 6 | 1 | FARP_MONEX | P41966 monelia ex  |
| 44 | 5 | 12.2 | 6 | 1 | TRPI_PSEPU | P36414 pseudomonas |
| 45 | 5 | 12.2 | 7 | 1 | CHOX_ALCSP | P16101 alcaigenes  |

## ALIGNMENTS

RESULT 1  
WMA2\_ACHFU STANDARD; PRT; 7 AA.  
AC P35920;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Wamide-2.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP  
RF TISSUE=Ganglion;  
RC MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
DR PIR; S33246; S33246.  
KW Neuropeptide; Amidation.  
FT MOD\_RES  
SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 41.5%; Score 17; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
||:  
Db 1 WKQ 3

RESULT 2  
WMA3\_ACHFU STANDARD; PRT; 7 AA.  
AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Wamide-3.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
CC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP  
RF TISSUE=Ganglion;  
RC MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108(1993).  
DR PIR; S33244; S33244.  
KW Neuropeptide; Amidation.

FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;  
 Query Match 41.5%; Score 17; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
 1 WKE 3

RESULT 3  
 BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 ID BPP7\_BOTIN  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide 55,2 (5A) (Angiotensin-converting  
 enzyme inhibitor)  
 OS Bothrops insularis (Island jararaca) (Queimada jararaca);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=9031557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 peptides from Bothrops insularis snake venom."  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -1- FUNCTION: This peptide both inhibits the activity of the  
 angiotensin-converting enzyme and enhances the action of  
 bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 CC PIR: G37196; G37196.  
 DR KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 5 AA; 623 MW; 776DC37326B00000 CRC64;

Query Match 39.0%; Score 16; DB 1; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
 2 KM 3

RESULT 4  
 WMA1\_ACHFV STANDARD; PRT; 7 AA.  
 ID WMA1\_ACHFV  
 AC P35919;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Wwamide-1.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wwamide-1", -2 and -3: novel neuromodulatory peptides isolated from  
 ganglia of the African giant snail, Achatina fulica."  
 RL FEBS Lett. 323:104-108(1993).  
 CC -1- FUNCTION: Exhibits modulatory effects on the peripheral nervous

CC system, inhibits activity on a central neuron.  
 DR PIR: S33245; S33245.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;  
 Query Match 34.1%; Score 14; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 WKX 7  
 1 WKE 3

RESULT 5  
 UF01\_MOUSE STANDARD; PRT; 5 AA.  
 ID UF01\_MOUSE  
 AC P38639;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=9500997; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins  
 using preparative two-dimensional gel electrophoresis."  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 protein is: 6.6, its MW is: 19 kDa.  
 CC NON\_TER 5  
 FT MOD\_RES 5  
 SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 31.7%; Score 13; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
 4 RW 5

RESULT 6  
 TY51\_LITRU STANDARD; PRT; 7 AA.  
 ID TY51\_LITRU  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Trypophyllin 5.1.  
 OS Iltoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyllidae;  
 OC Pelodyadinae; Iltoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steindorner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 Iltoria rubella". The skin peptide profile as a probe for the study  
 of evolutionary trends of amphibians."  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FPAB.  
 KW Amphibian defense peptide; Amidation; Neuropeptide;  
 KW Pyroglutamate carboxylic acid.  
 FT MOD RES 1 1 PYROGLUTAMATE CARBOXYLIC ACID.  
 FT MOD RES 7 7 AMIDATION.  
 SO SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 29.3%; Score 12; DB 1; Length 7;  
 Best Local Similarity 25.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 RMK 5  
 DB 1 QIPW 4

## RESULT 7

OCPS OCTMI STANDARD; PRT; 4 AA.  
 AC PS8643;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 CC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Necroleoidea;  
 CC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor.";  
 RL Peptides 21:623-630(2000).  
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less  
 CC active than Ocp-3.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: OCP-4 has D-Ser instead of L-Ser.  
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.  
 KW Hormone; D-amino acid.  
 FT MOD RES 2 2 D-SERINE (IN OCP-4).  
 SO SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 3 W 3

## RESULT 8

ID E101\_LITRU STANDARD; PRT; 6 AA.  
 AC P82056;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Electrin 1.  
 OS Litoria rubella (Desert tree frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 CC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;

RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 SO SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 5 W 5

## RESULT 9

ID LOK1\_LOCM1 STANDARD; PRT; 6 AA.  
 AC P41431;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Locustastakinin I.  
 OS Locusta migratoria (Migratory locust).  
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
 CC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=92262851; PubMed=1585017;  
 RA Schoof L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
 RA de Looz A.;  
 RT "Locustastakinin, a novel myotropic peptide from Locusta migratoria,  
 RT isolation, primary structure and synthesis.";  
 RL Regul. Pept. 37:49-57(1992).  
 CC -1- FUNCTION: Myotropic peptide. May be important in the stimulation  
 CC of ion transport and inhibition of diuretic activity in Malpighian  
 CC tubules.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC PIR; A61068; A61068.  
 KW Neuropeptide; Amidation.  
 FT MOD RES 6 6 AMIDATION.  
 SO SEQUENCE 6 AA; 654 MW; 666365A5B9CDB000 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 5 W 5

## RESULT 10

ID BRHP\_CONIM STANDARD; PRT; 7 AA.  
 AC P58603;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bromoheptapeptide Im.  
 OS Conus imperialis (Imperial cone).  
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 CC Apogastropoda; Caenogastropoda; Sorboconcha; Hypogastropoda;  
 CC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=35631;  
 RN [1]

## SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.

RC TISSUE=Venom; PubMed=9030520;  
 RX MEDLINE=9184108; Nielsen D.B., Guayas J.,  
 RA Craig A.G., Jimenez E.C., Dykert J.,  
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
 RA McIntosh J.M.;  
 RT "A novel post-translational modification involving bromination of  
 RT tryptophan. Identification of the residue, L-6-bromotryptophan, in  
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";  
 RL J. Biol. Chem. 272:4689-4694(1997).  
 CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected  
 CC centrally or peripherally in mice.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.  
 DR PIR, A58512; A58512;  
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.  
 FT DISULFID 2 7  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 6 6 BROMINATION.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 6 W 6

RESULT 11  
 TPEY PACDA STANDARD; PRT; 7 AA.  
 ID TPEY PACDA STANDARD; PRT; 7 AA.  
 AC P83455;

DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tryptophyltin-1 (Pdt-1).  
 OS Pachymedusa daemnicolor (Giant Mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 ON NCBI\_Taxid=75988;

RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
 RP PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;

RT "Pachymedusa daemnicolor tryptophyltin-1 (Pdt-1): structural  
 RT characterization, pharmacological activity and cloning of precursor  
 RT cDNA.";  
 RL Submitted (SEP-2002) to Swiss-Prote.  
 CC -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular  
 CC smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.

CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.

DR GO; GO:0005576; C:extracellular; NAS.

DR AM; GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.

KM Amphibian defense peptide; Amidation; Hydroxylation.

FT MOD\_RES 3 3 HYDROXYLATION.

FT MOD\_RES 7 7 AMIDATION.

SQ SEQUENCE 7 AA; 794 MW; 7772D37DC7776350 CRC64;

Query Match 26.8%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 W 5  
 DB 5 W 5

RESULT 12  
 VP19 HSV1K STANDARD; PRT; 6 AA.  
 ID VP19 HSV1K STANDARD; PRT; 6 AA.  
 AC P2310;

DT 01-NOV-1991 (Rel. 20, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Capsid assembly and DNA maturation protein (Viron protein U138)  
 DE (Capsid protein VP19C) (Fragment).  
 GN U138.

OS Herpes simplex virus (type 1 / strain XOS).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;

OC Alphaherpesvirinae; Simplexvirus.

ON NCBI\_Taxid=10306;

RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=91101287; Pubmed=1846198;  
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
 RA Silverstein S., Wagner E.K.;

RT "Analysis of the herpes simplex virus type 1 promoter controlling the  
 RT expression of U138, a true late gene involved in capsid assembly.";  
 RL J. Virol. 65:769-786(1991).

CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE  
 CC EMBEDDED. BINDS DNA.  
 CC -1- SIMILARITY: Belongs to the herpesviruses VP19C family.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL, M57646; AAA45830.1; -;  
 KW Capsid assembly; Coat protein; DNA-binding.  
 FT NON\_TER 6 6  
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 24.4%; Score 10; DB 1; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 MK 4  
 DB 1 MK 2

RESULT 13  
 FAR4\_HIRME STANDARD; PRT; 4 AA.  
 ID FAR4\_HIRME STANDARD; PRT; 4 AA.  
 AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRamide-like neuropeptide YMR-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Ahychrodeliida; Hirudiniformes; Hirudinidae; Hirudo.

ON NCBI\_Taxid=6421;

RN [1]

RP SEQUENCE

RX MEDLINE=92195954; Pubmed=1686933;

RA Evans B.D., Pohl U., Karstons M.A., Calabrese R.L.;

RT "Identification of Rfamide neuropeptides in the medicinal leech.";

RL Peptides 12:897-908(1991).

CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)  
 CC family.

KM Neuropeptide; Amidation.

FT MOD\_RES 4 4 AMIDATION.

SQ SEQUENCE 4 AA; 616 MW; 69D406B300000000 CRC64;

Query Match 19.5%; Score 8; DB 1; Length 4;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKW 5  
 DB 2 MRF 4

## RESULT 14

FMRP\_MACNI STANDARD; PRT; 4 AA.  
 ID FMRP\_MACNI  
 AC P01162;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE FMRPamide (peak C) (Cardioexcitatory neuropeptide).  
 OS Macrocallista nimbosa (Sun-ray clam).  
 OS Nereis virens (Sandworm).  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;  
 OC Veneroidea; Veneridae; Macrocallista.  
 OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and visceral ganglion;  
 RX MEDLINE=772155956; PubMed=877582;  
 RA Price D.A., Greenberg M.D.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide."  
 RL Science 197;670-671(1977).  
 RN [2]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
 RX MEDLINE=78012038; PubMed=909675;  
 RA Price D.A., Greenberg M.D.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc."  
 RL Prep. Biochem. 7;261-281(1977).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=N.virens;  
 RX MEDLINE=90259866; PubMed=2342992;  
 RA Kraigher K.G., Price D.A.;  
 RT "Authentic FMRPamide is present in the polychaete Nereis virens."  
 RL Peptides 11;75-77(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=H.medicalialis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamide neuropeptides in the medicinal leech."  
 RL Peptides 12;897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H.trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRPamide-related peptides from the kidney of the snail, Helisoma trivolvis."  
 RL Peptides 15;31-36(1994).  
 CC - FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.  
 CC - SIMILARITY: Belongs to the FMRP (FMRPamide related peptide) family.  
 DR PTR: A01426; ECKM.  
 DR PTR: A60418; A60418.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 4  
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 19.5%; Score 8; DB 1; Length 4;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKW 5  
 DB 2 MRF 4

## RESULT 15

FAR3\_HAECCO STANDARD; PRT; 7 AA.  
 ID FAR3\_HAECCO  
 AC P81298;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE FMRPamide-like neuropeptide PF3 (KSAVMRF-amide).  
 OS Haemonchus contortus (Barber pole worm).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyloida;  
 OC Trichostrongyloidea; Haemonchidae; Haemonchus.  
 OX NCBI\_TaxID=6289;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Neuron;  
 RX MEDLINE=99318264; PubMed=10391380;  
 RA Marks N.J., Sangster N.C., Maule A.G., Halton D.W., Thompson D.P.,  
 RA Geary T.G., Shaw C.;  
 RT "Structural characterisation and pharmacology of KHEVLRamide (AP2) and KSAVMRFamide (PF3/AF3) from Haemonchus contortus."  
 RL Mol. Biochem. Parasitol. 100;185-194(1999).  
 CC - FUNCTION: Active on neuromusculature.  
 CC - SIMILARITY: Belongs to the FMRP (FMRPamide related peptide) family.  
 CC Neuropeptide; Amidation.  
 KM Neuropeptide; Amidation.  
 FT MOD\_RES 7  
 SQ SEQUENCE 7 AA; 902 MW; 69D4068BDC55350 CRC64;

Query Match 19.5%; Score 8; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MKW 5  
 DB 5 MRF 7

Search completed: August 11, 2004, 14:08:46  
 Job time : 14 secs

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ID Q8GL00 PRELIMINARY; PRT; 7 AA.  
 AC Q8GL00;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE PF-50 protein (Fragment).  
 GN Borrelia burgdorferi (Lyme disease spirochete).  
 OG Plasmid group cp32-13.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CA15; Miller J.C.;  
 RA Stevenson B.;  
 RT "Comparative analyses of Borrelia burgdorferi erp genes and their cp32  
 RT prophages: conservation amidst diversity."  
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY142106; AAN17857.1; -  
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
 KM Plasmid.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 928 MW; 6337233050437350 CRC64;

Query Match 39.0%; Score 16; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
 DB 1 KW 2

RESULT 3  
 Q8KMS9 PRELIMINARY; PRT; 7 AA.  
 ID Q8KMS9;  
 AC Q8KMS9;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Putative transposase (Fragment).  
 GN TNA.  
 OS Enterobacter sp. CH2-4.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Enterobacter.  
 OX NCBI\_TaxID=143777;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CH2-4;  
 RC MEDLINE=21604134; PubMed=11763242;  
 RA Mirkin S.Z.; Kholodil G.V.; Gorlenko Z.M.; Minakhina S.V.;  
 RA Mirakhin L.S.; Kalyaeva E.S.; Kopeva A.V.; Petrova M.A.;  
 RA Yurleva O.V.; Nikiforov V.G.;  
 RT "Mercury resistance transposons of Gram-negative environmental  
 RT bacteria and their classification."  
 RL Res. Microbiol. 152:811-822(2001).  
 DR EMBL; AJ302778; CAC85058.1; -  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 966 MW; 737B1B1046DA9A0 CRC64;

Query Match 29.3%; Score 12; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KW 5  
 DB 6 EW 7

RESULT 4  
 ID P92214 PRELIMINARY; PRT; 7 AA.  
 AC P92214;

DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Amblyopyrum muticum.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Amblyopyrum.  
 OX NCBI\_TaxID=4595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H5572; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01346.1; -  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
 DB 5 RRL 7

RESULT 5  
 P92393 PRELIMINARY; PRT; 7 AA.  
 ID P92393;  
 AC P92393;  
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)  
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Ribosomal protein 11 (Fragment).  
 GN RPS11.  
 OS Hordeum vulgare (Barley).  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 OX NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H3139; TISSUE=Leaf;  
 RX MEDLINE=97271648; PubMed=9126564;  
 RA Petersen G.; Seberg O.;  
 RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
 RT sequence data."  
 RL Mol. Phylogenet. Evol. 7:217-230(1997).  
 DR EMBL; Z77756; CAB01370.1; -  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KM Chloroplast.  
 FT NON\_TER  
 SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
 DB 5 RRL 7

RESULT 6



RESULT 7  
P22403 PRELIMINARY; PRT; 7 AA.  
AC P22403;  
DT 01-MAY-1997 (TRENBLREL. 03, Created)  
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS *Lophopyrum elongatum* (Tall wheatgrass) (Aragopyrum elongatum).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticaceae; Thnopyrum.  
OC NCBI\_TaxID=4588;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6692; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticaceae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77743; CAB01307.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3  
||:  
Db 5 RRL 7

RESULT 7  
P22427 PRELIMINARY; PRT; 7 AA.  
ID P22427;  
AC P22427;  
DT 01-MAY-1997 (TRENBLREL. 03, Created)  
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Ribosomal protein (Fragment).  
GN RPS11.  
OS Peridictyon sanctum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticaceae; Peridictyon.  
OC NCBI\_TaxID=37683;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6575; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticaceae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77749; CAB01325.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3  
||:  
Db 5 RRL 7

RESULT 8  
P22430 PRELIMINARY; PRT; 7 AA.  
ID P22430;  
AC P22430;  
DT 01-MAY-1997 (TRENBLREL. 03, Created)  
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS *Aegilops tauschii* (Tausch's goatgrass) (Aegilops squarrosa).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticaceae; Aegilops.  
OC NCBI\_TaxID=37682;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H6668; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticaceae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77758; CAB01352.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3  
||:  
Db 5 RRL 7

RESULT 9  
P22221 PRELIMINARY; PRT; 7 AA.  
ID P22221;  
AC P22221;  
DT 01-MAY-1997 (TRENBLREL. 03, Created)  
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)  
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)  
DE Ribosomal protein 11 (Fragment).  
GN RPS11.  
OS Bromus inermis (Smooth brome grass).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Bromaceae; Bromus.  
OC NCBI\_TaxID=15371;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=OSA414; TISSUE=Leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.;  
RT "Phylogenetic analysis of the Triticaceae (Poaceae) based on rpoA  
sequence data."  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77759; CAB01355.1; -;  
DR GO; GO:0009507; C:chloroplast; IEA.  
KW Chloroplast.  
FT NON TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RRM 3  
||:  
Db 5 RRL 7

QY 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 10

ID P92425 PRELIMINARY; PRT; 7 AA.  
AC P92425;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Pseudoroegneria spicata (Bluebunch wheatgrass) (Agropyron spicatum).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Pseudoroegneria.  
OX NCBI\_TaxID=4604;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H9082; TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77744; CAB01310.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 11

ID P92381 PRELIMINARY; PRT; 7 AA.  
AC P92381;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Hordeum brachyantherum.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=52712;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77761; CAB01361.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 12

ID P92387 PRELIMINARY; PRT; 7 AA.  
AC P92387;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Henrardia petraea.  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Henrardia.  
OX NCBI\_TaxID=3676;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H5556; TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77748; CAB01322.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 13

ID P92210 PRELIMINARY; PRT; 7 AA.  
AC P92210;  
DT 01-MAY-1997 (TRENBLrel. 03, Created)  
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
GN Ribosomal protein 11 (Fragment).  
OS Agropyron cristatum (Crested wheatgrass).  
OC Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Agropyron.  
OX NCBI\_TaxID=4593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H4349; TISSUE=leaf;  
RX MEDLINE=97271648; PubMed=9126564;  
RA Petersen G., Seberg O.,  
RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA  
sequence data.";  
RL Mol. Phylogenet. Evol. 7:217-230(1997).  
DR EMBL; Z77771; CAB01391.1; -  
DR GO; GO:0009507; C:chloroplast; IEA.  
KM Chloroplast.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1e+06;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRM 3  
||:  
Db 5 RRL 7

## RESULT 14

ID P92440 PRELIMINARY; PRT; 7 AA.

AC P92440; 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

GN Ribosomal protein 11 (Fragment).

OS Thiopyrum bessarabicum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Thnopyrum.

NCBI\_TaxID=4601;

RP SEQUENCE FROM N.A.

RC STRAIN=H6725; TISSUE=Leaf;

RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G.; Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230 (1997).

DR EMBL; 277767; CAB01355.1; -

KW Chloroplast.

FT NON\_TER 1

SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRM 3  
||:  
Db 5 RRL 7

RESULT 15

ID P92218 PRELIMINARY; PRT; 7 AA.

AC P92218; 01-MAY-1997 (TREMBlrel. 03, Created)

DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

GN Ribosomal protein 11 (Fragment).

OS Thiopyrum bessarabicum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Austroalopyrum.

NCBI\_TaxID=4597;

RP SEQUENCE FROM N.A.

RC STRAIN=H6723; TISSUE=Leaf;

RX MEDLINE=97271648; PubMed=9126564;

RA Petersen G.; Seberg O.;

RT "Phylogenetic analysis of the Triticeae (Poaceae) based on rpoA

sequence data.";

RL Mol. Phylogenet. Evol. 7:217-230 (1997).

DR EMBL; 277767; CAB01379.1; -

DR GO; GO:0009507; C:chloroplast; IEA.

KW Chloroplast.

FT NON\_TER 1

SQ SEQUENCE 7 AA; 894 MW; 673414033277700 CRC64;

Query Match 29.3%; Score 12; DB 8; Length 7;

Best Local Similarity 66.7%; Pred. No. 1e+06;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRM 3  
||:  
Db 5 RRL 7

Search completed: August 11, 2004, 14:09:32

Job time : 36 secs

**This Page Blank (usp10)**

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: August 11, 2004, 14:02:18 ; Search time 50 Seconds  
(without alignments)  
39.557 Million cell updates/sec

Title: US-09-854-204-2  
Perfect score: 41  
Sequence: 1 RRMKWK 7  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 92273

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Jan04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2004s:\*  
8: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 41    | 100.0       | 7      | 3     | AAy83540 Peptide f |
| 2          | 41    | 100.0       | 7      | 3     | ADe14766 Carrier m |
| 3          | 41    | 100.0       | 7      | 3     | ADe14762 Drosophil |
| 4          | 41    | 100.0       | 7      | 5     | ABG15504 Fruit fly |
| 5          | 41    | 100.0       | 7      | 5     | AAE17558 Fluoresce |
| 6          | 41    | 100.0       | 7      | 5     | AAm48627 Anti-infl |
| 7          | 41    | 100.0       | 7      | 5     | AAm48620 Anti-infl |
| 8          | 41    | 100.0       | 7      | 6     | ABP60478 NLS pepit |
| 9          | 41    | 100.0       | 7      | 6     | ABP60478 NLS pepit |
| 10         | 41    | 100.0       | 7      | 6     | ADe11903 NFKB esse |
| 11         | 41    | 100.0       | 7      | 6     | ADe11896 NFKB esse |
| 12         | 41    | 100.0       | 7      | 7     | ADe11896 NFKB esse |
| 13         | 38    | 92.7        | 7      | 3     | AAy83544 Peptide f |
| 14         | 38    | 92.7        | 7      | 3     | AAy83543 Peptide f |
| 15         | 38    | 92.7        | 7      | 3     | ADe14767 Drosophil |
| 16         | 38    | 92.7        | 7      | 3     | ADe14766 Peptide f |
| 17         | 36    | 87.8        | 7      | 3     | AAy83546 Peptide f |
| 18         | 36    | 87.8        | 7      | 3     | AAy83539 Peptide f |
| 19         | 36    | 87.8        | 7      | 3     | ADe14769 Drosophil |
| 20         | 35    | 85.4        | 7      | 3     | AAy83547 Peptide f |
| 21         | 35    | 85.4        | 7      | 3     | ADe14770 Drosophil |
| 22         | 34    | 82.9        | 7      | 3     | AAy83545 Peptide f |
| 23         | 34    | 82.9        | 7      | 3     | ADe14768 Drosophil |
| 24         | 33    | 80.5        | 7      | 3     | AAy83549 Peptide f |
| 25         | 33    | 80.5        | 7      | 3     | ADe14772 Drosophil |

|    |      |      |   |   |                    |
|----|------|------|---|---|--------------------|
| 26 | 29   | 70.7 | 7 | 3 | AAy83550 Peptide f |
| 27 | 29   | 70.7 | 7 | 3 | ADe14773 Drosophil |
| 28 | 28   | 68.3 | 7 | 3 | AAy83548 Peptide f |
| 29 | 28   | 68.3 | 7 | 3 | ADe14771 Drosophil |
| 30 | 27   | 65.9 | 7 | 2 | AAw48057 AE14 sub  |
| 31 | 26   | 63.4 | 4 | 6 | ABR00891 Bioactive |
| 32 | 26   | 63.4 | 5 | 6 | ABR00892 Bioactive |
| 33 | 26   | 63.4 | 5 | 6 | AAw65537 Lipopept  |
| 34 | 25.5 | 62.2 | 7 | 3 | AAy83551 Peptide f |
| 35 | 25.5 | 62.2 | 7 | 3 | AAy83553 Peptide f |
| 36 | 25.5 | 62.2 | 7 | 3 | ADe14774 Drosophil |
| 37 | 25.5 | 62.2 | 7 | 3 | ADe14775 Drosophil |
| 38 | 25   | 61.0 | 7 | 2 | AAy21287 Human sem |
| 39 | 24   | 58.5 | 7 | 2 | AAw38781 Delivery  |
| 40 | 24   | 58.5 | 7 | 3 | AAy83552 Peptide f |
| 41 | 24   | 58.5 | 7 | 3 | AAy83554 Peptide f |
| 42 | 23   | 56.1 | 4 | 2 | AAw43242 Peptide f |
| 43 | 23   | 56.1 | 5 | 5 | AAE21734 BSMR esse |
| 44 | 23   | 56.1 | 6 | 2 | AAy1352 Antimicro  |
| 45 | 23   | 56.1 | 6 | 2 | AAy1353 Antimicro  |

## ALIGNMENTS

RESULT 1  
ID AAY83540 standard; peptide; 7 AA.  
XX AC AAY83540;  
XX DT 29-AUG-2000 (first entry)  
XX DE Peptide fragment of membrane transport vector penetratin.  
XX DE Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
XX KW conjugate; vector.  
XX KM  
XX OS Synthetic.  
XX PN W0200029427-A2.  
XX PD 25-MAY-2000.  
XX PE 11-NOV-1999; 99WO-G8003750.  
XX PR 13-NOV-1998; 98GB-00025000.  
XX PR 13-NOV-1998; 98GB-00025001.  
XX PR 04-FEB-1999; 99GB-00002522.  
XX PR 04-FEB-1999; 99GB-00002525.  
XX PR 22-JUN-1999; 99GB-00014578.  
XX PA (CYCL-) CYCLACEL LTD.  
XX PI Fischer MF, Zhelev N;  
XX DR WPI, 2000-387734/33.  
XX PT New membrane translocation peptide carrier group for delivering  
XX PT therapeutic agents into target cells comprises specified sequence of  
XX PT amino acids.  
XX PS Claim 5; Page 26; 59pp; English.  
XX CC Penetratin is a membrane translocation polypeptide and as such, active  
XX CC peptide fragments of penetratin can be used to translocate conjugated  
XX CC molecules across the cell membrane e.g. drugs, 13 chemical entities are  
XX CC described for use in the method such as paclitaxel-  
XX CC 2'-succinimidopropionyl-Cbetar-RRMKWK-NH<sub>2</sub>, and podophylotoxin-4-  
XX CC succinimidopropionyl-Cbetar-RRMKWK-NH<sub>2</sub>. The method has applications as  
XX CC a drug delivery system for treatment and therapy. The resulting  
XX CC conjugated molecules exhibit high immunogenicity, solubility and  
XX CC clearance. The penetratin peptide fragment may be truncated and or have

CC amino acid substitutions. See GENESSEQ records AAY83520-Y83581

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 2

ID ADE14786 standard; peptide; 7 AA.

AC ADE14786;

DT 29-JAN-2004 (first entry)

DE Carrier moiety SeqID26 related to improved drug delivery.

KM drug delivery system; carrier group; homeobox peptide; drug metabolism;  
KM drug biodistribution; drug excretion; drug half life; drug solubility;  
KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
KM fruit fly; mutant; mutein.

OS Synthetic.

OS Drosophila melanogaster.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Optionally C-terminal H"  
FT Modified-site 7 /note= "N-terminal amide"

PN WO200001417-A1.

PD 13-JAN-2000.

PF 22-JUN-1999; 99WO-GB001957.

PR 03-JUL-1998; 98GB-00014527.

PA (CYCL-) CYCLACEL LTD.

PI Fischer PM, Wang S;

DR WPI; 2000-160729/14.

PT Delivery systems with improved delivery into target cells, half-life, solubility in biological fluids, enhanced metabolism, biodistribution and excretion, and minimal toxic side-effects.

PS Claim 33; SEQ ID NO 26; 114bp; English.

XX This invention relates to novel drug delivery systems comprising a drug group linked to a carrier group comprising a homeobox peptide, its fragment or derivative. The invention may provide a method of improved delivery into target cells with enhanced metabolism, biodistribution and excretion of a drug. The drug may be therapeutically active in both intact and dissociated states. The invention may improve half-life of a drug in human or animal bodies, improve solubility in biological fluids, minimize known toxic or non-desirable side-effects, enhance onset of action of a desired therapeutic effect, provide alternative routes for administration of drug and decrease incidence of drug resistance. The present sequence is the amino acid sequence of a carrier peptide derived from penatrin, a peptide derived from the antennapedia homeodomain of Drosophila melanogaster. The drug and carrier moieties associated with this sequence in the exemplification of the invention are featured.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 3

ID ADE14762 standard; peptide; 7 AA.

AC ADE14762;

DT 29-JAN-2004 (first entry)

DE Drosophila melanogaster homeodomain truncated penatrin peptide SeqID2.

KM drug delivery system; carrier group; homeobox peptide; drug metabolism;  
KM drug biodistribution; drug excretion; drug half life; drug solubility;  
KM drug side-effect; drug resistance; penatrin; antennapedia homeodomain;  
KM fruit fly.

OS Drosophila melanogaster.

PN WO200001417-A1.

PD 13-JAN-2000.

PF 22-JUN-1999; 99WO-GB001957.

PR 03-JUL-1998; 98GB-00014527.

PA (CYCL-) CYCLACEL LTD.

PI Fischer PM, Wang S;

DR WPI; 2000-160729/14.

PT Delivery systems with improved delivery into target cells, half-life, solubility in biological fluids, enhanced metabolism, biodistribution and excretion, and minimal toxic side-effects.

PS Claim 9; SEQ ID NO 2; 114bp; English.

XX This invention relates to novel drug delivery systems comprising a drug group linked to a carrier group comprising a homeobox peptide, its fragment or derivative. The invention may provide a method of improved delivery into target cells with enhanced metabolism, biodistribution and excretion of a drug. The drug may be therapeutically active in both intact and dissociated states. The invention may improve half-life of a drug in human or animal bodies, improve solubility in biological fluids, minimize known toxic or non-desirable side-effects, enhance onset of action of a desired therapeutic effect, provide alternative routes for administration of drug and decrease incidence of drug resistance. The present sequence is the amino acid sequence of a truncated form of penatrin, a peptide derived from the antennapedia homeodomain of Drosophila melanogaster, which is related to the invention.

XX Sequence 7 AA;

Query Match 100.0%; Score 41; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7  
| | | | |  
DB 1 RRMKKKK 7

RESULT 4

ABG75504  
ID ABG75504 standard; peptide; 7 AA.  
AC ABG75504;  
XX  
XX  
DT 14-APR-2003 (first entry)  
XX  
XX  
DE Fruit fly Antp-HD truncated membrane translocation sequence #2.  
XX  
XX Translocation; delivery vehicle; agent-membrane translocation sequence;  
XX MTS; membrane translocation sequence; plasma membrane; red blood cell;  
XX immunisation; antigen; intracellular delivery; therapeutic; HIV-1;  
XX trans-activating protein; Tat; Antennapedia homeodomain protein; Antp-HD;  
XX VP22 protein; HSV-VP22; signal-sequence-based peptide; Transportin;  
XX Amphiphilic model peptide; Fruit fly.  
XX  
XX Drosophila sp.  
XX  
XX US2002151004-A1.  
XX  
XX 17-OCT-2002.  
XX  
XX 16-FEB-2001; 2001US-00785802.  
XX  
XX 24-JUL-2000; 2000WO-G8002848.  
XX 09-AUG-2000; 2000WO-G8003056.  
XX 22-DEC-2000; 2000US-00748063.  
XX 22-DEC-2000; 2000US-00748789.  
XX  
XX (CRAI/) CRAIG R.  
XX  
XX Craig R;  
XX  
XX MPI; 2002-260593/32.  
XX  
XX Preparing a red blood cell vehicle suitable for delivering an agent to a  
XX target site in a vertebrate due to loading the red blood cell with an  
XX agent-membrane translocation sequence.  
XX  
XX  
XX Disclosure; Page 8; 43pp; English.  
XX  
XX The invention discloses a method for preparing a delivery vehicle for  
XX delivering an agent to a target site in a vertebrate. The method  
XX comprises loading a cell with an agent-membrane translocation sequence  
XX (MTS) conjugate, which contains a membrane translocation sequence  
XX enabling the agent to cross the plasma membrane of a cell. Also disclosed  
XX is a pharmaceutical composition comprising a red blood cell for delivery  
XX of an agent to a vertebrate, the red blood cell comprising the novel  
XX agent-MTS conjugate and a method of immunisation of an animal with an  
XX antigen. The method is useful for preparing delivery vehicles,  
XX particularly a red blood cell, for the intracellular delivery of a  
XX therapeutic agent to a target site. The method is particularly useful for  
XX enabling an agent to cross the plasma membrane of a target cell, and for  
XX selectively releasing the agent-MTS conjugate at a target site to  
XX facilitate the uptake of the agent by the cells at the target site. The  
XX preferred MTS sequences are from HIV-1 transactivating protein (Tat),  
XX Drosophila Antennapedia homeodomain protein (Antp-HD), Herpes Simplex-1  
XX virus VP22 protein (HSV-VP22), a signal-sequence-based peptide and a  
XX Transportin and Amphiphilic model peptide. The sequence presented is the  
XX active truncated Fruit fly MTS, #2  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AAE17558  
ID AAE17558 standard; peptide; 7 AA.  
AC AAE17558;  
XX  
XX  
DT 22-APR-2002 (first entry)  
XX  
XX  
DE Fluorescent timer fusion proteins constructing NLS peptide #16.  
XX  
XX Fluorescent timer protein; protein movement; translocation; trafficking;  
XX promoter activity; gene expression; transgenic plant; gene modification;  
XX protein age; nuclear localisation signal; NLS.  
XX  
XX Unidentified.  
XX  
XX WO200196373-A2.  
XX  
XX 20-DEC-2001.  
XX  
XX 13-JUN-2001; 2001WO-US019097.  
XX  
XX 14-JUN-2000; 2000US-0211607P.  
XX  
XX (CLON-) CLONTECH LAB INC.  
XX  
XX Fradkov AF, Tersikh A;  
XX  
XX MPI; 2002-154595/20.  
XX  
XX  
XX New fluorescent timer proteins comprising an emission spectrum that  
XX changes over time from a first wavelength to a second wavelength, useful  
XX for monitoring intracellular protein movement, translocation, trafficking  
XX or stability.  
XX  
XX  
XX Disclosure; Page 18; 89pp; English.  
XX  
XX The invention relates to a fluorescent timer protein having an emission  
XX spectrum that changes over time after synthesis from a first wavelength  
XX to a second wavelength. The fluorescent timer proteins are useful in  
XX monitoring the activity of a promoter, determining the age of a protein,  
XX identifying an agent that modulates the activity of a promoter and in  
XX enriching a population of cells comprising a fluorescent timer protein.  
XX The fluorescent timer proteins are also useful for assessing gene  
XX expression during development of a multicellular organism or during  
XX cellular differentiation, in response to a drug or other inducer of  
XX promoter activity, as a reporter to serve as a read-out of promoter  
XX activity, monitoring intracellular protein movement or translocation,  
XX protein trafficking, or protein stability, to investigate temporal  
XX aspects of the activity of a regulatory element, for determining cell  
XX fate during development and organ remodelling, in spatial and temporal  
XX visualisation of newly synthesised proteins and accumulated proteins, and  
XX in distinguishing between newly formed and pre-existing structures, e.g.  
XX membrane junctions and extracellular matrix components. The fluorescent  
XX timer proteins may further be used to investigations where photobleaching  
XX techniques are employed, as detectable labels, as selectable markers, as  
XX biosensors in prokaryotic and eukaryotic cells, in protease cleavage  
XX assays, and as second messenger detectors. The nucleic acids can be used  
XX to generate transgenic, non-human plants or animals or site-specific gene  
XX modifications in cell lines. The present sequence is nuclear localisation  
XX signal (NLS) peptide used for constructing fluorescent timer proteins  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 41; DB 5; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AA48627 standard; peptide; 7 AA.  
 ID AA48627;  
 AC AA48627;  
 XX  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 130.  
 XX  
 XX  
 KW Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014346.  
 XX  
 PR 02-MAY-2000; 2000US-0201261P.  
 PR 22-AUG-2000; 2000US-00643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 DR  
 XX  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.  
 XX  
 PS Claim 11; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AA48628-AA48645), comprising a membrane translocation domain (AA48620-  
 CC AA48627 or AA48646-AA48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AA48525-AA48619). The  
 CC antiinflammatory compounds have antiaesthetic, cyostatic, antipsoriatic,  
 CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antithrombotic, virucide and antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis  
 CC  
 SQ Sequence 7 AA;  
 XX  
 Query Match 100.0%; Score 41; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
 |||||

Db 1 RRMKKK 7  
 RESULT 7  
 AA48620  
 ID AA48620 standard; peptide; 7 AA.  
 XX  
 XX  
 AC AA48620;  
 XX  
 XX  
 DT 20-MAR-2002 (first entry)  
 XX  
 XX  
 DE Anti-inflammatory peptide SEQ ID NO 123.  
 XX  
 XX  
 KW Anti-inflammatory; antiaesthetic; cyostatic; antipsoriatic; nootropic;  
 KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;  
 KW immunosuppressive; dermatological; neuroprotective; antithrombotic;  
 KW antiallergic; membrane translocation domain; NEMO binding domain; eczema;  
 KW cytokine; NF-kappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;  
 KW rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;  
 KW autoimmune disorder; multiple sclerosis; transplant rejection;  
 KW osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;  
 KW ataxia telangiectasia; allergy; anaphylaxis; arthritis.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200183554-A2.  
 XX  
 PD 08-NOV-2001.  
 XX  
 PF 02-MAY-2001; 2001WO-US014346.  
 XX  
 PR 02-MAY-2000; 2000US-0201261P.  
 PR 22-AUG-2000; 2000US-00643260.  
 XX  
 PA (PRAE-) PRACIS PHARM INC.  
 PA (UYVA) UNIV YALE.  
 PI May MJ, Ghosh S, Findeis MA, Phillips K;  
 PI WPI; 2002-121889/16.  
 DR  
 XX  
 XX  
 PT Novel antiinflammatory compound comprising membrane translocation domain  
 PT fused to NEMO binding sequence, useful for blocking nuclear factor kappaB  
 PT activation, and for treating asthma, lung inflammation, psoriasis.  
 XX  
 PS Claim 11; Page 62; 88pp; English.  
 XX  
 CC The invention relates to an antiinflammatory compound (especially  
 CC AA48628-AA48645), comprising a membrane translocation domain (AA48620-  
 CC AA48627 or AA48646-AA48651) which comprises from 6-15 amino acid  
 CC residues, fused to a NEMO binding sequence (AA48525-AA48619). The  
 CC antiinflammatory compounds have antiaesthetic, cyostatic, antipsoriatic,  
 CC antirheumatic, antiarthritic, osteopathic, antibacterial,  
 CC immunosuppressive, dermatological, neuroprotective, nootropic,  
 CC antithrombotic, virucide and antiallergic activity. The compounds  
 CC act as selective inhibitors of cytokine-mediated NF-kappaB activation by  
 CC blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding  
 CC domain that results in inhibition of IKKbeta kinase activation and  
 CC subsequent decreased phosphorylation of IkappaB. The compounds are useful  
 CC for treating inflammatory disorders, e.g. asthma, lung inflammation or  
 CC cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory  
 CC bowel disease, sepsis, vasculitis, bursitis, autoimmune diseases such as  
 CC lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;  
 CC transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;  
 CC viral infections; and ataxia telangiectasia. The compounds are also  
 CC useful for treating pro-inflammatory responses such as allergies,  
 CC urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,  
 CC sunburn, aging and arthritis  
 CC  
 SQ Sequence 7 AA;  
 XX  
 Query Match 100.0%; Score 41; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;



Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
| | | | |  
ID 1 RRMKMK 7

RESULT 8  
ABP60478  
ID ABP60478 standard; peptide; 7 AA.

XX ABP60478;  
XX  
XX 10-MAY-2003 (first entry)  
XX  
XX NLS peptide SEQ ID NO 17.  
XX  
XX Protease; detection; drug screening; caspase; apoptosis; infection;  
XX nuclear localisation signal; NLS.  
XX  
XX Unidentified.  
XX  
XX WO2003012393-A2.  
XX  
XX 13-FEB-2003.

XX 30-JUL-2002; 2002WO-US024119.  
XX  
XX 31-JUL-2001; 2001US-0309112P.  
XX  
XX (CLON-) CLONTECH LAB INC.  
XX  
XX Haugwitz M;  
XX  
XX WPI; 2003-248202/24.

PT Detecting the presence of active protease in a cell for use in protease  
PT activity detection and drug screening applications, by using a protease  
PT detection fusion protein.  
XX  
XX  
XX Disclosure; Page 10; 43pp; English.

XX The invention relates to a cell comprising a protease detection fusion  
XX protein containing first and second subcellular localisation domains (D1,  
XX D2) separated by a cleavage domain (CD) recognised by the protease,  
XX (where D1 is dominant over D2 and a label domain is present between CD  
XX and D2). The fusion protein is maintained for a period of time sufficient  
XX for CD to be cleaved by protease if present in the cell and subcellular  
XX localisation of label domain is detected. The method is useful for  
XX determining whether a cell contains an active protease. The method finds  
XX applications, including monitoring activity of a protease in a cell,  
XX monitoring the effect of an agent on the activity of a protease, e.g. for  
XX drug screening applications to identify agents that modulate the activity  
XX of a particular protease and studying the effect of a factor on  
XX expression of the protease-encoding gene. Detecting protease activity of  
XX interest in a cell is useful for determining the particular state of the  
XX cell associated with the particular protease, e.g. certain active  
XX caspases indicate that a cell is undergoing an apoptotic event. Protease  
XX detection applications can be used in diagnostic applications, including  
XX diagnosis of bacterial and/or viral pathogenic infection. The present  
XX sequence is that of a nuclear localisation signal (NLS) containing  
XX peptide disclosed in illustrations of the invention

XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
| | | | |  
ID 1 RRMKMK 7

RESULT 9  
ABP6972  
ID ABP6972 standard; peptide; 7 AA.

XX ABP6972;  
XX  
XX 17-JUN-2003 (first entry)  
XX  
XX  
XX Anti-inflammatory polybasic peptide SEQ ID NO:11.

XX Anti-inflammatory; inflammatory disorder; polybasic; antiallergic;  
XX cytoskeletal; tuberculostatic; nephrotoxic; antineoplastic; antiallergic;  
XX dermatological; immunosuppressive; antiallergic; antiparasitic; asthma;  
XX gynaecological; ophthalmological; chromolytic; protein therapy;  
XX lung inflammation; cancer; chronic granulomatous disease; tuberculosis;  
XX leprosy; sarcoidosis; silicosis; nephritis; rheumatoid arthritis;  
XX amyloidosis; ankylosing spondylitis; chronic bronchitis; scleroderma;  
XX lupus; appendicitis; psoriasis; pelvic inflammatory disease; allergy;  
XX orbital inflammatory disease; thrombotic disease.

XX Synthetic.  
XX  
XX WO2003020213-A2.  
XX  
XX 13-MAR-2003.

XX 27-AUG-2002; 2002WO-US027421.  
XX  
XX 30-AUG-2001; 2001US-0316328P.  
XX  
XX (PRAE-) PRAECIS PHARM INC.

XX Lazarus D, Hannig G;  
XX  
XX WPI; 2003-354457/33.

PT New polybasic peptide useful for treating inflammatory disorders, such as  
PT asthma, lung inflammation, cancer, chronic granulomatous diseases,  
PT nephritis, amyloidosis, rheumatoid arthritis, scleroderma or allergies.  
XX  
XX  
XX Claim 34; Page 23; 35pp; English.

XX The present invention describes an anti-inflammatory compound comprising  
XX a polybasic peptide (I). (I) comprises the structure: B1-X1-X2-X3-B2-X4-  
XX X5-B3, or B1-X1-X2-B2-B3-X3-X4-B4, where B1, B2, B3 and B4 = basic amino  
XX acid residues; and X1, X2, X3, X4 and X5 = alpha-helix promoting amino  
XX acid residues. Also described: (1) methods of treating an inflammatory  
XX disorder in a subject; and (2) a method for modulating the secretion of  
XX pro-inflammatory cytokines in a cell. (1) has cytostatic,  
XX antiinflammatory, antiallergic, tuberculostatic, nephrotoxic,  
XX antipneumatic, antiallergic, dermatological, immunosuppressive,  
XX antiallergic, antiparasitic, gynaecological, ophthalmological and  
XX thrombolytic activities, and can be used in protein therapy. The  
XX composition and method are useful in treating inflammatory disorders,  
XX such as asthma, lung inflammation, cancer, chronic granulomatous diseases  
XX (e.g. tuberculosis, leprosy, sarcoidosis or silicosis), nephritis,  
XX amyloidosis, rheumatoid arthritis, ankylosing spondylitis, chronic  
XX bronchitis, scleroderma, lupus, appendicitis, psoriasis, pelvic  
XX inflammatory disease, orbital inflammatory disease, thrombotic disease  
XX and allergies. The present sequence represents a specifically claimed  
XX anti-inflammatory polybasic peptide from the present invention

XX  
SQ Sequence 7 AA;

Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMK 7  
| | | | |  
ID 1 RRMKMK 7

RESULT 10  
ADA61903  
ID ADA61903 standard; peptide; 7 AA.  
XX  
AC ADA61903;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #103.  
XX  
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiaesthetic; antipsoriatic; antirheumatic;  
KW antirheumatic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuromodulatory; cytosolic; nocitropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYN/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDEIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 11; Page 24; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (1). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
DB 1 RRMKKK 7

RESULT 11  
ADA61896  
ID ADA61896 standard; peptide; 7 AA.  
XX

AC ADA61896;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE NFkB essential modulator (NEMO) binding peptide #96.  
XX  
KW NEMO binding domain; NBD; I kappa B kinase beta; IKKbeta;  
KW antiinflammatory; antiaesthetic; antipsoriatic; antirheumatic;  
KW antirheumatic; osteopathic; antibacterial; immunosuppressive;  
KW dermatological; neuromodulatory; cytosolic; nocitropic; virucide;  
KW gene therapy; anti-inflammatory; inflammatory disorder; asthma;  
KW psoriasis; rheumatoid arthritis; osteoarthritis;  
KW inflammatory bowel disease; sepsis; vasculitis; autoimmune disease;  
KW systemic lupus erythematosus; multiple sclerosis; cancer; osteoporosis;  
KW Alzheimer's disease; viral infection; NF-kappa B essential modulator;  
KW necrosis factor kappa B essential modulator.  
XX  
OS Unidentified.  
XX  
PN US2003054999-A1.  
XX  
PD 20-MAR-2003.  
XX  
PF 02-MAY-2001; 2001US-00847946.  
XX  
PR 02-MAY-2000; 2000US-0201261P.  
XX  
PA (MAYN/) MAY M J.  
PA (GHOS/) GHOSH S.  
PA (FIND/) FINDEIS M A.  
PA (PHIL/) PHILLIPS K.  
PA (HANN/) HANNIG G.  
XX  
PI May MJ, Ghosh S, Findeis MA, Phillips K, Hannig G;  
XX  
DR WPI; 2003-596541/56.  
XX  
PT New compound for diagnosing or treating inflammatory disorders, e.g.  
PT asthma, psoriasis, rheumatoid arthritis, inflammatory bowel disease or  
PT cancer, comprises a membrane translocation domain and a NEMO binding  
PT sequence.  
XX  
PS Claim 11; Page 24; 37pp; English.  
XX  
CC The invention describes an anti-inflammatory compound comprising (1). The  
CC compound is useful for diagnosing or treating inflammatory disorders,  
CC such as asthma, psoriasis, rheumatoid arthritis, osteoarthritis,  
CC inflammatory bowel disease, sepsis, vasculitis, autoimmune diseases (e.g.  
CC systemic lupus erythematosus), multiple sclerosis, cancer, osteoporosis,  
CC Alzheimer's disease or viral infection. This is the amino acid sequence  
CC of an anti-inflammatory peptide that binds to, and down-regulates,  
CC necrosis factor kappa B (NFkB) essential modulator (NEMO).  
XX  
SQ Sequence 7 AA;  
XX  
Query Match 100.0%; Score 41; DB 6; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKK 7  
DB 1 RRMKKK 7

RESULT 12  
ADC22330  
ID ADC22330 standard; peptide; 7 AA.  
XX  
AC ADC22330;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Nuclear localization signal motif amino acid sequence SEQ ID NO:179.

XX recombinant fusion protein; fusion protein; binding; detection;  
 KW localization domain; binding domain;  
 KM subcellular compartment localisation.  
 XX  
 OS Unidentified.  
 XX  
 PN WO2003012068-A2.  
 XX  
 PD 13-FEB-2003.  
 XX  
 PF 01-AUG-2002; 2002WO-US024572.  
 XX  
 PR 01-AUG-2001; 2001US-030939SP.  
 PR 13-DEC-2001; 2001US-0341589P.  
 XX  
 PA (CELL-) CELLONICS INC.  
 XX  
 PI Bright G, Premkumar DR, Chen Y;  
 DR WPI; 2003-248174/24.  
 XX  
 XX New recombinant fusion protein comprising detection and first  
 PT localization domains and a binding domain for the molecule of interest.  
 PT useful for detecting binding of a molecule of interest.  
 PT  
 PS Claim 20; SEQ ID NO 179; 101pp; English.  
 XX  
 CC The present invention describes a recombinant fusion protein (I) for  
 CC detecting binding of a molecule of interest. (I) comprises: (a) a  
 CC detection domain; (b) a first localisation domain; and (c) a binding  
 CC domain for the molecule of interest. The detection domain, the first  
 CC localisation domain and the binding domain for the molecule of interest  
 CC constituting the recombinant fusion protein for detecting binding of a  
 CC molecule of interest are operably linked. The binding domain for the  
 CC molecule of interest is separated from the first localisation domain by 0  
 CC -20 amino acid residues. The first localisation domain and the binding  
 CC domain for the molecule of interest both do not occur in a single non-  
 CC recombinant protein with the same spacing as in the recombinant fusion  
 CC protein for detecting binding of a molecule of interest. Also described:  
 CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;  
 CC (2) a recombinant expression vector comprising the nucleic acid control;  
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a  
 CC genetically engineered host cell transfected with the recombinant  
 CC expression vector; (4) a kit for detecting binding of the molecule of  
 CC interest; and (5) a method for identifying compounds that alter the  
 CC binding of the molecule of interest. The recombinant fusion protein is  
 CC useful for detecting binding of a molecule of interest. The recombinant  
 CC fusion protein eliminates the need to construct two or more chimeric  
 CC proteins and enables the monitoring of biochemical events in live, intact  
 CC or fixed cells. The present sequence is used in the exemplification of  
 CC the present invention.  
 CC  
 SQ Sequence 7 AA;  
 XX  
 XX  
 Query Match 100.0%; Score 41; DB 7; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWKX 7  
 | | | | | | |  
 DB 1 RRMKWKX 7  
 RESULT 13  
 ID AAY83544 standard; peptide; 7 AA.  
 AC AAY83544;  
 XX  
 XX 29-AUG-2000 (first entry)  
 DT  
 XX  
 DE Peptide fragment of membrane transport vector penetratin.

XX Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KW conjugate; vector.  
 KM  
 XX Synthetic.  
 OS  
 XX WO200029427-A2.  
 PN  
 XX 25-MAY-2000.  
 PD  
 XX 11-NOV-1999; 99WO-GB003750.  
 PF  
 XX 13-NOV-1998; 98GB-00025000.  
 PR 13-NOV-1998; 98GB-00025001.  
 PR 04-FEB-1999; 99GB-00002522.  
 PR 04-FEB-1999; 99GB-00002525.  
 PR 22-JUN-1999; 99GB-00014578.  
 XX  
 PA (CYCL-) CYCLACEL LTD.  
 XX  
 PI Fischer MP, Zhelev N;  
 DR WPI; 2000-387734/33.  
 XX  
 XX New membrane translocation peptide carrier group for delivering  
 PT therapeutic agents into target cells comprises specified sequence of  
 PT amino acids.  
 PT  
 PS Claim 7; Page 26; 59pp; English.  
 XX  
 CC Penetratin is a membrane translocation polypeptide and as such, active  
 CC peptide fragments of penetratin can be used to translocate conjugated  
 CC molecules across the cell membrane e.g. drugs. 13 chemical entities are  
 CC described for use in the method such as paclitaxel-  
 CC 2-succinimidopropionyl-Cbeta-RMKK-NH<sub>2</sub>, and podophylotoxin-4-  
 CC succinimidopropionyl-Cbeta-RMKK-NH<sub>2</sub>. The method has applications as  
 CC a drug delivery system for treatment and therapy. The resulting  
 CC conjugated molecules exhibit high immunogenicity, solubility and  
 CC clearance. The penetratin peptide fragment may be truncated and or have  
 CC amino acid substitutions. See GENESQ records AAY83520-Y83581  
 CC  
 SQ Sequence 7 AA;  
 XX  
 XX  
 Query Match 92.7%; Score 38; DB 3; Length 7;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RRMKWKX 7  
 | | | | | | |  
 DB 1 RRMKWKX 7  
 RESULT 14  
 ID AAY83543 standard; peptide; 7 AA.  
 AC AAY83543;  
 XX  
 XX 29-AUG-2000 (first entry)  
 DT  
 XX  
 DE Peptide fragment of membrane transport vector penetratin.  
 KW Penetratin; translocation; membrane; drug delivery; therapy; treatment;  
 KM conjugate; vector.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200029427-A2.  
 PD  
 XX 25-MAY-2000.  
 PF  
 XX 11-NOV-1999; 99WO-GB003750.  
 PR



Wed Aug 11 15:15:11 2004

us-09-854-204-2.closed.rapb

Page 1

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OM protein - protein search, using sw model

Run on: August 11, 2004, 14:09:35 ; Search time 41 Seconds

(without alignments)  
53.597 Million cell updates/sec

Title: US-09-854-204-2

Perfect score: 41

Sequence: 1 RRMKWK 7

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 51202

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
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14: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID                 | Description        |
|------------|-------|-------------|--------|-----------------------|--------------------|
| 1          | 41    | 100.0       | 7      | 9 US-09-854-204-2     | Sequence 2, Appl1  |
| 2          | 41    | 100.0       | 7      | 9 US-09-785-802A-6    | Sequence 6, Appl1  |
| 3          | 41    | 100.0       | 7      | 10 US-09-847-946A-123 | Sequence 123, App  |
| 4          | 41    | 100.0       | 7      | 10 US-09-847-946A-130 | Sequence 130, App  |
| 5          | 41    | 100.0       | 7      | 12 US-10-144-549-4    | Sequence 4, Appl1  |
| 6          | 41    | 100.0       | 7      | 12 US-10-228-915-11   | Sequence 11, Appl1 |
| 7          | 41    | 100.0       | 7      | 14 US-10-211-088-179  | Sequence 179, App  |
| 8          | 41    | 100.0       | 7      | 14 US-10-210-660-2    | Sequence 2, Appl1  |
| 9          | 41    | 100.0       | 7      | 14 US-10-210-660-26   | Sequence 26, Appl1 |
| 10         | 41    | 100.0       | 7      | 14 US-10-315-920-22   | Sequence 22, Appl1 |
| 11         | 38    | 92.7        | 7      | 9 US-09-854-204-9     | Sequence 9, Appl1  |
| 12         | 38    | 92.7        | 7      | 9 US-09-854-204-10    | Sequence 10, Appl1 |
| 13         | 38    | 92.7        | 7      | 14 US-10-210-660-6    | Sequence 6, Appl1  |
| 14         | 38    | 92.7        | 7      | 14 US-10-210-660-7    | Sequence 7, Appl1  |
| 15         | 36    | 87.8        | 7      | 9 US-09-854-204-12    | Sequence 12, Appl1 |

|    |      |      |   |                       |                    |
|----|------|------|---|-----------------------|--------------------|
| 16 | 36   | 87.8 | 7 | 9 US-09-854-204-55    | Sequence 55, Appl1 |
| 17 | 36   | 87.8 | 7 | 14 US-10-210-660-9    | Sequence 9, Appl1  |
| 18 | 35   | 85.4 | 7 | 9 US-09-854-204-4     | Sequence 4, Appl1  |
| 19 | 35   | 85.4 | 7 | 14 US-10-210-660-10   | Sequence 10, Appl1 |
| 20 | 34   | 82.9 | 7 | 9 US-09-854-204-11    | Sequence 11, Appl1 |
| 21 | 34   | 82.9 | 7 | 14 US-10-210-660-8    | Sequence 8, Appl1  |
| 22 | 33   | 80.5 | 7 | 9 US-09-854-204-14    | Sequence 14, Appl1 |
| 23 | 33   | 80.5 | 7 | 14 US-10-210-660-12   | Sequence 12, Appl1 |
| 24 | 29   | 70.7 | 7 | 9 US-09-854-204-15    | Sequence 15, Appl1 |
| 25 | 29   | 70.7 | 7 | 14 US-10-210-660-13   | Sequence 13, Appl1 |
| 26 | 28   | 68.3 | 7 | 9 US-10-462-452-790   | Sequence 790, App  |
| 27 | 28   | 68.3 | 7 | 14 US-10-210-660-11   | Sequence 11, Appl1 |
| 28 | 27   | 65.9 | 7 | 11 US-09-261-894-135  | Sequence 135, App  |
| 29 | 26   | 63.4 | 4 | 9 US-09-854-204-66    | Sequence 66, App   |
| 30 | 26   | 63.4 | 4 | 10 US-09-820-053A-133 | Sequence 133, App  |
| 31 | 26   | 63.4 | 4 | 14 US-10-109-171-133  | Sequence 133, App  |
| 32 | 26   | 63.4 | 5 | 10 US-09-820-053A-134 | Sequence 134, App  |
| 33 | 26   | 63.4 | 5 | 14 US-10-109-171-134  | Sequence 134, App  |
| 34 | 26   | 63.4 | 6 | 9 US-09-765-614B-19   | Sequence 19, Appl1 |
| 35 | 26   | 63.4 | 6 | 9 US-09-925-715-8     | Sequence 8, Appl1  |
| 36 | 26   | 63.4 | 6 | 16 US-10-722-075-19   | Sequence 19, Appl1 |
| 37 | 26   | 63.4 | 7 | 9 US-09-854-204-3     | Sequence 3, Appl1  |
| 38 | 25.5 | 62.2 | 7 | 9 US-09-854-204-16    | Sequence 16, Appl1 |
| 39 | 25.5 | 62.2 | 7 | 9 US-09-854-204-17    | Sequence 17, Appl1 |
| 40 | 25.5 | 62.2 | 7 | 14 US-10-210-660-14   | Sequence 14, Appl1 |
| 41 | 25.5 | 62.2 | 7 | 14 US-10-210-660-15   | Sequence 15, Appl1 |
| 42 | 24   | 58.5 | 7 | 9 US-09-854-204-5     | Sequence 5, Appl1  |
| 43 | 24   | 58.5 | 7 | 9 US-09-854-204-18    | Sequence 18, Appl1 |
| 44 | 24   | 58.5 | 7 | 9 US-09-854-204-19    | Sequence 19, Appl1 |
| 45 | 24   | 58.5 | 7 | 9 US-09-805-301-95    | Sequence 95, Appl1 |

#### ALIGNMENTS

RESULT 1  
US-09-854-204-2  
; Sequence 2, Application US/09854204  
; Patent No. US20020098236A1  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Peter Martin  
; APPLICANT: Zhelev, Nikolaï  
; TITLE OF INVENTION: Transport Vectors  
; FILE REFERENCE: CCI-010  
; CURRENT APPLICATION NUMBER: US/09/854,204  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 09/438,460  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: GB 9825000.4  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: GB 9825001.2  
; PRIOR FILING DATE: 1998-11-13  
; PRIOR APPLICATION NUMBER: GB 9902525.6  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: GB 9902522.3  
; PRIOR FILING DATE: 1999-02-04  
; PRIOR APPLICATION NUMBER: GB 9914578.1  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: PCT/GB99/03750  
; PRIOR FILING DATE: 1999-11-11  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; NAME/KEY: MOD RES  
; LOCATION: (7)  
; OTHER INFORMATION: AMIDATION, the carboxy terminal lysine residue may have its carboxyl group converted into an

OTHER INFORMATION: carboxamide group.  
US-09-854-204-2

Query Match 100.0%; Score 41; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

RESULT 2

US-09-785-802A-6  
Sequence 6, Application US/09785802A  
Patent No. US20020151004A1  
GENERAL INFORMATION:  
APPLICANT: Craig, Roger  
TITLE OF INVENTION: DELIVERY VEHICLES AND METHODS FOR USING THE SAME  
FILE REFERENCE: 11067/2035  
CURRENT APPLICATION NUMBER: US/09/785,802A  
PRIOR FILING DATE: 2001-02-16  
PRIOR APPLICATION NUMBER: US 09/748,06  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US 09/748,789  
PRIOR FILING DATE: 2000-12-22  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-09-785-802A-6

Query Match 100.0%; Score 41; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

RESULT 3

US-09-847-946A-123  
Sequence 123, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Funder, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 123  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:membrane  
OTHER INFORMATION: translocation domain  
US-09-847-946A-123

Query Match 100.0%; Score 41; DB 10; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

RESULT 4  
US-09-847-946A-130  
Sequence 130, Application US/09847946A  
Publication No. US20030054999A1  
GENERAL INFORMATION:  
APPLICANT: May, Michael J  
APPLICANT: Ghosh, Sankar  
APPLICANT: Funder, Mark A  
APPLICANT: Phillips, Kathryn  
TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF  
FILE REFERENCE: PPI-119  
CURRENT APPLICATION NUMBER: US/09/847,946A  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: 60/201,261  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: 09/643,260  
PRIOR FILING DATE: 2000-08-22  
NUMBER OF SEQ ID NOS: 160  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 130  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:membrane  
OTHER INFORMATION: translocation domain  
US-09-847-946A-130

Query Match 100.0%; Score 41; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

RESULT 5  
US-10-144-549-4  
Sequence 4, Application US/10144549  
Publication No. US20030211590A1  
GENERAL INFORMATION:  
APPLICANT: Genescribe Biopharm, Inc.  
APPLICANT: Hsu, Paul L.  
TITLE OF INVENTION: A NEW FUSION PROTEIN FOR USE AS VECTOR  
FILE REFERENCE: MBHB 02-340  
CURRENT APPLICATION NUMBER: US/10/144,549  
PRIOR FILING DATE: 2002-05-13  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 4  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Drosophila melanogaster  
US-10-144-549-4

Query Match 100.0%; Score 41; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRMKWK 7  
Db 1 RRMKWK 7

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RESULT 6
US-10-229-915-11
; Sequence 11, Application US/10229915
; Publication No. US20030083262A1
; GENERAL INFORMATION:
; APPLICANT: Lazarus, Douglas
; APPLICANT: Hamnig, Gerhard
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING INFLAMMATORY
; TITLE OF INVENTION: DISORDERS
; FILE REFERENCE: FPI-127
; CURRENT APPLICATION NUMBER: US/10/229,915
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/316,328
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: anti-inflammatory compound
US-10-229-915-11

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 1 RRMKKKK 7

RESULT 7
US-10-211-088-179
; Sequence 179, Application US/10211088
; Publication No. US20030104479A1
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular B
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 179
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-179

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 1 RRMKKKK 7

RESULT 8
US-10-210-660-2
; Sequence 2, Application US/10210660
; Publication No. US20030119735A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; APPLICANT: Wang, Shudong
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/10/210,660
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US/09/346,847
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-210-660-2

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 1 RRMKKKK 7

RESULT 9
US-10-210-660-26
; Sequence 26, Application US/10210660
; Publication No. US20030119735A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, M. Peter
; APPLICANT: Wang, Shudong
; TITLE OF INVENTION: Delivery System
; FILE REFERENCE: CCI-009
; CURRENT APPLICATION NUMBER: US/10/210,660
; CURRENT FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US/09/346,847
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: GB 9814527
; PRIOR FILING DATE: 1998-07-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)_RES
; OTHER INFORMATION: AMIDATION
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-210-660-26

Query Match          100.0%; Score 41; DB 14; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKKKK 7
Db 1 RRMKKKK 7

RESULT 10
US-10-315-920-22
; Sequence 22, Application US/10315920
```

Publication No. US20030175809A1  
GENERAL INFORMATION:  
APPLICANT: Tradkov, Arcady Fedorovich  
APPLICANT: Terexikh, Alexey  
TITLE OF INVENTION: FLUORESCENT TIMER PROTEINS AND METHODS  
TITLE OF INVENTION: FOR THEIR USE  
FILE REFERENCE: CLON-077CIP  
CURRENT APPLICATION NUMBER: US/10/315,920  
CURRENT FILING DATE: 2002-12-09  
PRIOR APPLICATION NUMBER: 60/211,607  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: PCT/US01/19097  
PRIOR FILING DATE: 2001-06-13  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: nuclear localization signal  
US-10-315-920-22

Query Match 100.0%; Score 41; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 11  
US-09-854-204-9  
Sequence 9, Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikola  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-854-204-9

Query Match 92.7%; Score 38; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7

DB 1 RRMKWK 7

RESULT 12  
US-09-854-204-10  
Sequence 10, Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikola  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-854-204-10

Query Match 92.7%; Score 38; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKWK 7  
DB 1 RRMKWK 7

RESULT 13  
US-10-210-660-6  
Sequence 6, Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
APPLICANT: Wang, Shudong  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-6



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US-10-210-660-6

Query Match 92.7%; Score 38; DB 14; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
DB 1 KRMKMKK 7

RESULT 14  
US-10-210-660-7  
Sequence 7; Application US/10210660  
Publication No. US20030119735A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, M. Peter  
APPLICANT: Wang, Shudong  
TITLE OF INVENTION: Delivery System  
FILE REFERENCE: CCI-009  
CURRENT APPLICATION NUMBER: US/10/210,660  
CURRENT FILING DATE: 2002-07-31  
PRIOR APPLICATION NUMBER: US/09/346,847  
PRIOR FILING DATE: 1999-07-02  
PRIOR APPLICATION NUMBER: GB 9814527  
PRIOR FILING DATE: 1998-07-03  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-210-660-7

Query Match 92.7%; Score 38; DB 14; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
DB 1 KRMKMKK 7

RESULT 15  
US-09-854-204-12  
Sequence 12; Application US/09854204  
Patent No. US20020098236A1  
GENERAL INFORMATION:  
APPLICANT: Fischer, Peter Martin  
APPLICANT: Zhelev, Nikolai  
TITLE OF INVENTION: Transport Vectors  
FILE REFERENCE: CCI-010  
CURRENT APPLICATION NUMBER: US/09/854,204  
CURRENT FILING DATE: 2001-05-11  
PRIOR APPLICATION NUMBER: 09/438,460  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: GB 9825000.4  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9825001.2  
PRIOR FILING DATE: 1998-11-13  
PRIOR APPLICATION NUMBER: GB 9902525.6  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9902522.3  
PRIOR FILING DATE: 1999-02-04  
PRIOR APPLICATION NUMBER: GB 9914578.1  
PRIOR FILING DATE: 1999-06-22  
PRIOR APPLICATION NUMBER: PCT/GB99/03750  
PRIOR FILING DATE: 1999-11-11  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 12  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-854-204-12

Query Match 87.8%; Score 36; DB 9; Length 7;  
Best Local Similarity 85.7%; Pred. No. 1.2e+06;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RRMKMKK 7  
DB 1 RRMKMKK 7

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Job time : 42 secs

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